From:

Whiteman, Brian

Sent:

Thursday, November 10, 2005 10:35 AM

To:

STIC-Biotech/ChemLib

Subject:

seq search

10/696,282 Wilson et al.

SEQ ID NO: 13, 15, and 17 and

nucleotides 335 to 2272 of SEQ ID NO: 1 and nucleotides 1007 to 2272 of SEQ ID NO: 1:

- 1) search against us issued and published us patent database
- 2) commercial databases

thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

HOV TO 2003

Searcher:	_
Searcher Phone:	
Date Searcher Picked up:	
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Т	ype of	Search	
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Structure	#:	Text:	_
Inventor		Litigation:	

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LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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From:

Whiteman, Brian

Sent:

Thursday, November 10, 2005 10:41 AM STIC-Biotech/ChemLib

To: Subject:

seq search

10/696,900 Wilson et al.

nucleotides 1 to 143 of SEQ ID NO: 1; nucleotides 4576-4718 of SEQ ID NO: 1; nucleotides 2223-4431 of SEQ ID NO: 1; nucleotides 2829-4432 of SEQ ID NO: 1

- 1) search against us issued and published us patent database
- 2) commercial databases

thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

HALE NK

Searcher:
Searcher Phone:
Date Searcher Picked up:
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Inventor:	Litigation

Vendors and cost where applicable STN:\_\_ DIALOG: QUESTEL/ORBIT:
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## SUMMARIES

Descri Aay711 Abb80 Abr62 Ade76 Adv70 Adz277		ADE76566 Ade765	ADZ27070 Adz270	ADZ27086 Adz270	ADZ27010 Adz270				
Description Aay71167 Ad Abb80232 AA Abb80236 Ad Abr62762 Ad Ade76565 Ad Ade770294 Pr Ad227010 Ad		566 Ade76566	Z27070 Adz27070		ADZ27086 AdZ27086				

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Adz26992	Adz26996	Adz26965	Adz26951	Adz26962	Adz26966	Adz27034	Ade76600	Adz26963	Ade76599	Ade76597	Adz27080	Adv67508	Ade76601	Abr62764	Abb80229	Adz26960	Ade76598	Adz27085	Adz26959	Adz27067
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## ALIGNMENTS

RESULT 1
AAY71167
ID AAY7 Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; VP1. Adeno-associated virus serotype 1 capsid protein VP1. 08-SEP-2000 (first entry) AAY71167 standard; protein; 736 AA. WO200028061-A2. AAY71167; 05-NOV-1998; 02-NOV-1999; 18-MAY-2000. Adeno-associated virus 1. (UYPE-) UNIV PENNSYLVANIA. 98US-0107114P 99WO-US025694.

Wilson JM, Xiao W;

WPI; 2000-376571/32. N-PSDB; AAD00772, AAD00777.

Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.

Claim 7; Page 87-90; 108pp; English.

The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a

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RESULT 2
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Matches 736
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            AAV1
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                                                                          ABB80232
           vp1 protein
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New isolated adeno-associated virus (AAV) comprising an AAV9 useful for preparing a medicament for delivering a transgene
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                                                                                                                                                                            17-DEC-2001;
05-JUN-2002;
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    capsid,
to a cell.
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The sequences given in ABB80231-34 represent vpl proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three proteins vpl, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene to a cell

Disclosure; Fig 2; 76pp; English.

Sequence 736 Ä

Matches

736;

Local Similarity

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Score 3989; DB 6; Pred. No. 4.9e-311; ); Mismatches 0;

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                                                                           The present sequence is the protein sequence of the vpl capsid protein of adeno associated virus serotype 1 (AAVI). The invention provides the nucleic acid and amino acid sequences of novel AAV8 and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cells. Among the desirable fragments are the cap proteins, including vpl, vp2, vp3 and hypervariable regions, the rep proteins, including rep70, rep68, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination with other AAV8 sequences or in combination with elements from other AAV or non-AAV viral sequences in the production of recombinant AAV and for use as antisense delivery vectors, gene therapy vectors or vaccine vectors. A claimed molecule comprises a cap protein of a functional AAV rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.
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                                                          rep gene
AAV6
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01-MAY-2002;
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2002US-0377133P
2002US-0386122P
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Matches
                   adeno-associated virus; AAV; cytostatic; antipsoriatic; an antiarthritic; neuroprotective; antidiabetic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
                                                                                                                                                              ADE76565 standard;
                                                                                         Adeno-associated virus (AAV)
                                                                                                                                        ADE76565;
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            thyroiditis;
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                                                                                            related protein,
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17-DEC-2001;
01-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antipsoriatic, antithyeunatic, antiarthritic, neuroprotective, antidiabetic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This sequence represents an AAV related protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFBEVP
                                                          INNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
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                                                                                                                  TTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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; 2001US-0341117P.
; 2002US-0377066P.
; 2002US-0386675P.
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ilarity 100.0%;
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Pred. No. 4.9e-311;
; Mismatches 0;
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                                                                                                     EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
                                                                                                                                                                          ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA
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                           YTEPRPIGTRYLTRPL
YTEPRPIGTRYLTRPL
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ADV70294 standard; protein; 736

10-MAR-2005

(first

entry)

Primate adeno-associated virus 1 capsid protein VP1.

RESULT 5
ADV702947
XX ADV77
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XX ADV77
XX ADV77
XX ADV77
XX ADV77
XX Frimmu
XX Immu
XX Hemo
XX Crig
XX Hemo
XX WO20
XX Inmm.
XX WO11
XX New
XX Nex
XX Ne immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia; Pepck deficiency; galactosemia; phenylketonuria; Crigior-Najjar syndrome; Gout; Zellweger syndrome; hechemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder; muscular dystrophy; diabetes; VP1.

Adeno-associated virus

29-DEC-2004

21-JUN-2004; 2004WO-US019884

19-JUN-2003; 30-APR-2004; 03-JUN-2004; 2003US-0480395P 2004US-0567310P 2004US-0576501P

(AVIG-) AVIGEN INC

Colosi ٣ Lochrie ₹, Surosky

2005-048755/05

New mutated adeno-associated virus (AAV) capsid protein that when pin an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating hemophilia. e.g.

IJ ğ 20; 136pp; English

The invention describes a mutated adeno-associated protein that when present in an AAV virion imparts immunoreactivity to the virion as compared to the virion. Also described are: a polynucleotide encodi described are: a polynucleotide encoding sociated virus (AAV) (
imparts decreased
to the corresponding the mutated capsid wild-type ed protein

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CC above; a recombinant AAV virion comprising the mutated protein above; and Cd delivering a recombinant AAV virion to a cell or tissue of a vertebrate CC subject. The recombinant AAV virion is useful for delivering a CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate CC molecule is expressed at a level that provides a therapeutic effect, CC where the recombinant AAV virion may comprise a non-primate, mammalian CC immunoreactivity to the virion as compared to immunoreactivity to the virion as compared to immunoreactivity of primate cC nucleic acid molecule encodes a therapeutic protein and is operably CC linked to control elements capable of directing the in vivo transcription and translation of the protein. The protein or the recombinant AAV virion and translation of the protein a wide variety of disorders such as themphilia, glycogen storage deficiency type 1A, Pepck deficiency, CC galactosemia, phenyletenouria, Crigler-Najjar disease, Gout and Lesch-CC Nyan syndrome, Zellweger syndrome, ischemic diseases, atherosclerosis, CC cancer, inflammatory and immune disorders, muscular dystrophies, and CC diabetes. This is the amino acid sequence of adeno-associated virus 1 cc (AAVI) capsid protein VP1.
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                                               ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA 660
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EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
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                                                                                                                                       The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; e
virucide; antibacterial; cytostatic; antiulcer; dermatological
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                                                                                                                                                                                                                                                                                                                                                sclerosis, diabetes, scleroderma, infection and cancer.
                                                                                                                                                                                                                                                                                                                                                                 New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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29-APR-2004; 2004US-0566546P.
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WAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
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                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; antiulcer;
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                                                         Score 3989; DB 9;
Pred. No. 4.9e-311;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                psoriasis,
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  30-SEP-2003; 2003US-0508226P
                                                 30-SEP-2004;
                                                                                                                                                                                                       Adeno-associated
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Matches 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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                                                                               GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                                                                                                                        INNNWGFRFKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLFYVLGSAHQ
                                                                                                                                                                                                     TTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
                   FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
                                                              GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                                                                                                                                                                      TTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRL
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Matches 735
                                                                                                                                                                                                                                                            The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoB) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV7) or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents a cappid protein of AAV serotype 1 (AAV1), which may be used in recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an AAV serotype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
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                                                                                                                                            MIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
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30-JUN-2005

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rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinflammatory, antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; antipsoriatic; vasotropic; gastrointestinal-gen.; virucide; antibacterial; Adeno-associated virus protein SEQ ID NO Adeno-associated virus neuroprotective; antiinflammatory; antidiabetic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV; bacterial; cytostatic; antiulcer; dermatological. cytostatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an adeno-associated virus (AAV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial infection and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
                                                                                         FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP
                                                                                                                                                      GCLPPFPADVFMI PQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                                                                                                                                                                                                  INNNWGFRPKRLNFKLFNIQVEEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 157; 569pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2004US-0566546P.
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Pred. No. 2.4e-309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 10
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                                                                                                          Query Match
Best Local S
Matches 730
                                                                                                                                                                                                                                                              The present invention relates to adeno-associated virus serotypes. The present sequence is capsid protein VPI of one such serotype (AAV6). AAV6 can be used to contruct AAV viral vectors for use in gene therapy for a range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis, sickle cell anaemia, thalassaemia, blood clotting disorders and diabetes. The AAV viral vectors have increased transduction efficiency of a particular host cell as the AAV virion containing the AAV vector genome can be modified to express a capsid protein of an AAV serotype that transduces the selected host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV6; gene therapy; AAV viral vector; cystic fibrosis; cancer; AIDS; atherosclerosis; sickle cell anaemia; thalassaemia; blood clotting disorder; diabetes; capsid protein VP1.
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome, sickle cell anemia, thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-060164/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59847;
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  MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 2; 50pp; English.
                                                                                                             Conservative
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                                                                                                          Score 3963; DB 4;
Pred. No. 6.1e-309;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                   adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004
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                                12-NOV-2002; 2002EP-00257826
                                                                                    14-MAY-2003
                                                                                                                                           EP1310571-A2
                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                          autoimmune thyroiditis; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus (AAV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA
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Best Local Similarity
Matches 730; Conserv
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17-DEC-2001;
01-MAY-2002;
05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ត្
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PR 13-NOV-2001; 2001US-0350607P.
PR 17-DEC-2001; 2001US-0341117P.
PR 01-MAY-2002; 2002US-0386675P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX (UYPE-) UNIV PENNSYLVANI
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The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample concaining a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cycostatic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other aucoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This sequence represents an AAV related protein sequence of the invention.

Q sequence 736 AA;
Query Match 99.3%; Score 3963; DB 7; Length 736;
Best Local Similarity 99.2%; Pred. No. 6.1e-309;
Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Matches 730; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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γ	1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60	_
DЬ	1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60	-
Qy •	61 KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120	Ö
Db	61 KGEPVNAADAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120	Ö
δ	121 AKKRYLEPLGLYEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE 180	ö
DЬ	121 AKKRVLEPPGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE 180	ö
Ş	181 SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI 240	0
Db	181 SVPDPQPLGEPPATPAAVGPTTWASGGGAPMADNNEGADGVGNASGNWHCDSTWLCDRVI 240	0
8	241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDENRFHCHFSPRDWQRL 300	ŏ
Db	241 TTSTRTWALPTYNNHLYKQISSASTGASNDNHYEGYSTPWGYFDFNRFHCHFSPRDWQRL 300	ŏ
Qy	360 INNNWGERPKRLNFKLENIQVKEVTTNDGVTTTANNLTSTVQVFSDSEYQLPYVLGSAHQ 360	ŏ
Вb	301 INNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ 360	ŏ
Qy	361 GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP 420	ŏ
Db	361 GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVP 420	ŏ
Qy	421 FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLP 480	õ
Ф	421 FHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNXDLLFSRGSPAGMSVQPXXWLP 480	õ
Ş	481 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINDGTAMASHKDDEDKFFPMSGV 540	6

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RESULT 12
ADV70293
ADV70293
AXX ADV70
XX ADV70
XX ADV70
XX Inmur
XX Inmur
XX Inmus
XX Inmus
XX Aden
XX Aden
XX Aden
XX AD
PD 29-D
XX AD
PD 29-D
XX AD
PR 19-J
PR 19-J
PR 19-J
PR 30-J
PR 30-J
PR 19-J

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The invention describes a mutated adeno-associated virus (AAV) capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion. Also described are: a polymucleotide encoding the mutated protein above; a recombinant AAV virion comprising the mutated protein above; and delivering a recombinant AAV virion to a cell or tissue of a vertebrate subject. The recombinant AAV virion is useful for delivering a heterologous nucleic acid molecule to a cell or tissue of a vertebrate subject, where the protein encoded by the heterologous nucleic acid molecule is expressed at level that provides a therapeutic effect, where the recombinant AAV virion may comprise a non-primate, mammalian AAV capsid protein that when present in an AAV virion imparts decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutated adeno-associated virus (AAV) in an AAV virion imparts decreased immur compared to the corresponding wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia; Pepck deficiency; galactosemia; phenylketonuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                Example 5; SEQ
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30-APR-2004; 2004US-0567310P.
03-JUN-2004; 2004US-0576501P.
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                                                       BFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
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                                       EFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTV
                                                                                                    ALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPPA
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Pred. No. 6.1e-309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease, hemophilia, HIV, pacterial intercolitis. The present sequence represents adeno-associated virus protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADZ27070 standard;
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antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
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29-APR-2004; 2004US-0566546P.
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SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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                                                                                AKKRVLEPFGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
                                                                                                               AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
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                           ABFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG
                                                                                   PFHSSYAHSQSLDRLMNFLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSBYQLPYVLGSAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITTSTRTWALPTYNNHLYKQISSASTGASNONHYFGYSTPWGYFDFNRFHCHFSPRDWQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESVPDPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV
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                                                                                                                                                                        VMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM
                                                                                                                                                                                                        VMIFGKESAGASNTALDNVMITDEEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM
                                                                                                                                                                                                                                                                                           PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                       QGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGEPVNAADAAALEHDKAYDQQLKAGDNPYPRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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AEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSASVDFTVDNNG
                                                                                                                                                                                                                                                                PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESI INPGTAMASHKDDEDKPFPMSG
                                                                                                                                                                                                                                                                                                                                               PLHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer.
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97.7%;
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Pred. No. 1.1e-303;
6; Mismatches 10;
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                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative coltis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; HIV; sacterial infection; cancer; ulcerative colitis; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacter
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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29-APR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virucide; antibacterial; cytostatic; antiulcer; dermatological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adeno-associated virus protein
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                                                                                                                                                                                                                                                                                                Local
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                                                                                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
                                                                                                                                                           MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
                                                                                                                                                                                                                                                                                                                                                                              737
                                                       KGEPVNAADAAALEHDKAYDQQLKAGDNPYPRYNHADAEFQERLQEDTPFGGNLGRAVFQ
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2004US-0566546P
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97.4%;
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В	γ	Db	Ş	망	φ	DЬ	8	망	Ş	рb	Ş	Db	Ş	DЬ	γQ	DЪ	Ş	οь	Q	В
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LYTEPRPIGTRYLIRPL 737	LYTEPREIGTRYLTRPL 736	AEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSASVDFTVDNNG 720	AEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG 719	GALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPP 660	GALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPP 659	WIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM 600	VMIFGKESAGASNTALDNVMITDEEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAM 599	PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG 540	PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG 539	PLHSSYAHSQSLDRLMNPLIVQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL 480	PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWL 479	QCCLPPFPADVEMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEV 420	QGCLPPFPADVEMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTPBEV 419	CLENIQVKEVTTNDGV	LINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAH 359	ITTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQR 300	ITTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTDWGYFDFNRFHCHFSPRDWQR 299	ESVPDPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV 240	ESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV 239	

Search completed: November 23, 2005, 17:35:10 Job time: 134.527 secs

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        pred. No. is the number of results predicted by chance to have a
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

4: . /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: ^/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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      Match Length
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      BB
    US-09-807-802A-3
US-09-807-802A-13
US-09-321-589-1
US-10-293-478-1
US-10-293-478-1
US-10-038-972A-13
US-09-807-802A-17
US-10-038-972A-14
US-09-532-594B-16
US-09-533-427-4
US-09-533-427-6
US-09-856-841-116
US-08-856-841-19
US-08-856-841-19
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Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 29, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 18, Appli Sequence 29, Appli Sequence 29, Appli Sequence 21, Appl
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2.9	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.1	3.1	ω 	3.6	3.6	3.6	4.8	5.4	7.1	7.6
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Sequence 7, Appl	Sequence 3855, Ar	Sequence 2, Appl:	Sequence 2, Appl	Sequence 2, Appl	Sequence 2, Appli	Sequence 2, Appli		Sequence 14, Appl	Sequence 14, App	Sequence 4, Appl	Sequence 12, Appl	•	Sequence 9, Appl	Sequence 2, Appl	Patent No. 52342		Sequence 21, App

## ALIGNMENTS

35AHQ 360	301 INNNWGFRÞKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSBYQLÞYVLGSAHQ	Q Y
<u> </u>	241 TISTRIWALPIYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRL 	\$ 8
	181 SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI 	B 8
G _ G	121 AKKRYLEPLGIVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE 	B 8
ZAVE	61 KGEPVNAADAAALEHDKAYDOOLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 	B 8
T GL	1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQOKQDDGRGLVLPGYKYLGPPNGLD 	유 성
	LENGTH: 736  TYPE: PRT ORGANISM: AAV-1 -09-807-802A-3  100.0%; Score 3989; DB 2; Length 736; Query Match	(X)
	FILE REFERENCE: GNVPN.031USA CURRENT APPLICATION NUMBER: US/09/807,802A CURRENT FILING DATE: 2002-02-21 PRIOR APPLICATION NUMBER: US 60/107,114 PRIOR FILING DATE: 1998-11-05 PRIOR FILING DATE: 1998-11-05 PRIOR APPLICATION NUMBER: PCT/US99/25694 PRIOR FILING DATE: 1999-11-02 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin version 3.1	•
Sequences	US-09-807-802A-3 ; Sequence 3, Application US/09807802A ; Patent No. 6759237 ; GENERAL INFORMATION: ; APPLICANT: Wilson, James M. ; APPLICANT: Xiao, Weidong ; TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid ; TITLE OF INVENTION: Vectors and Host Cells Containing Same	US-09-8 ; Seque ; Paten ; GENER ; GENER ; APPL ; APPL ; TITL ; TITL

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; ORGANISM: AAV-1
US-09-807-802A-13
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TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR PRILING DATE: 1998-11-05
PRIOR PRILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 736
TYPE. DBT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/09807802A Patent No. 6759237 GENERAL INFORMATION:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 736; Conserv
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SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
                                                                        AKKRVLEPLGLVEEGAKTAPGKKRPVEQS PQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
                                                                                                                                            KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
                                                                                                                                                                                          MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD
                                                                                                                                                                                                            MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPPNGLD
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                                                     AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE
                                                                                                                       KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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; LENGTH: 735
; TYPE: PRT
; ORGANISM: Adeno-associated virus
US-09-321-589-1
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Patent No. 6498244
GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
FILE REFERENCE: 39672
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/09/321,589
CURRENT PILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
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Matches 61
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                                                                                                                                                                                                                            Similarity
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                        AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSE 180
                                                                       KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ
                                                                                        KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
                                                                                                                                        MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD
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       AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGQQPARKRLNFGQTGDAD
                                                                                                                                                                                                          85.3%; Score 3402.5; DB 2;
larity 83.3%; Pred. No. 7.2e-290;
Conservative 51; Mismatches 71;
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GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CA
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/10/293,478
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/321,589
PRIOR FILING DATE: 1999-05-28
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 613; Conserv
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Adeno-associated virus
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KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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                                                               MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD
                                                                                                                                                  85.3%; Score 3402.5; DB 2; llarity 83.3%; Pred. No. 7.2e-290; Conservative 51; Mismatches 71;
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                                                                                                                                                                      Sequence 13, Application US/10038972A

Patent No. 6962815

Patent No. 6962815

PAPLICANT: J. Bartlett

ITITLE OF INVENTION: AAV VECTORS AND METHODS

FILE REFERENCE: 28335/36996US

CURRENT APPLICATION NUMBER: US/10/038,972A

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: US 60/260,124

PRIOR APPLICATION NUMBER: US 60/260,124

PRIOR FILING DATE: 2001-01-05

NUMBER OF EGO ID NOS: 18

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 735

TYPE: PRT

ORGANISM: adeno-associated virus 2 VP1 caspid protien
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                                                                         Conservative
                                                                      85.3%; Score 3402.5; DB 2; 83.3%; Pred. No. 7.2e-290; tive 51; Mismatches 71;
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600 539 540 479

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RESULT 6
US-09-807-802A-15
US-09-807-802A-15; Sequence 15, Application US/09807802A; Patent No. 6759237;
                                              TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GUVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
LENGTH: 599
TYPE: PRT
ORGANISM: AAV-1
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                                                                                                                                                                                                                                                                                       James M.
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                                                   ; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-17
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US-09-807-802A-17
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                                                                                                     APPLICANT: Wilson, James M.
APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT FILING DATE: 1902-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application Patent No. 6759237
Query Match
Best Local Similarity
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72.9%;
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Score 2906; DB 2;
Pred. No. 1.8e-246;
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                    Length 534;
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GENERAL INFORMATION:
APPLICANT: J. BATTLETE
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-038-972A-14
                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 598
TYPE: PRT
ORGANISM: adeno-associated virus 2 VP2 capsid protien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10038972A Patent No. 6962815
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                                                                                                                                                                                         Match 69.2%; Score 2759.5; DB 2;
Local Similarity 82.8%; Pred. No. 1.7e-233;
heb 495; Conservative 43; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVITINDGVTTI ANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736
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QISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFN 318
                                                                                                                      PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
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                                                      GTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYK
                                                                    GPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYK 258
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APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THER
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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US-09-532-594B-4
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                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP1 US-09-532-594B-4
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Best Local S
Matches 475
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                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 734
TYPE: PRT
ORGANISM: Artificial
FEATURE:
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                            123
                                                                                                                                                                                                                              tch 62.3%; Score 2486.5; DB 2; al Similarity 63.5%; Pred. No. 2.3e-209; 475; Conservative 81; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDQYLYYLNRTQNQSGSAQNKDLLESRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNN
                                                                                                                                                         VSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 598
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                          RVLEPLGLVEQAGETAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGP
                                            RVLEBLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESV 182
                                                                                                             PVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKK
                                                                                           PVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQAKK
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GENERAL INFORMATION:
APPLICANT: J. BARTLETE
INTLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-10-038-972A-15
; Sequence 15, Application
; Patent No. 6962815
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TYPE: PRT
; ORGANISM: adeno-associated virus 2 VP3 capsid protien
US-10-038-972A-15
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                            263 ASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322
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                                                                                             MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNWLPGPCYROORVSKTKTDNNNSNFTWTGAS---KY----NLNGRESIINPGTAMASHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFHSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTN----FTKLRPTNFSNFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQN----QSGSAQNKDLLFSRGSPAGMSVQP
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              QS-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                           Conservative
                                                                                                                                                         62.2%; Score 2481.5; 83.3%; Pred. No. 3.7
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                                                                                                                                           Mismatches
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Davidson, Elizabeth
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
ITILE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRJ
FILE REFERENCE: 14014,0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
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US-09-533-427-4
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4
LENGTH: 724
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                                                                                                                                                                                                                                                       Matches 431;
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 72
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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QLQIPAQPASSLGADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRT
                  LGEPPATPA-AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRT 246
                                                                                                                                           ADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVE
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                                                             PFGLVEEGAKTAPTGKRIDDHFPKRKKART-----EEDSKP----STSSDAEAGPSGSQ 176
                                                                                           PLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQP
                                                                                                                            ADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLE
                                                                                                                                                                                        PDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNA
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                                                                                                                                                                                                                                                                                                                                      Description of Artificial synthetic construct
                                                                                                                                                                                                                                                                      58.6%;
                                                                                                                                                                                                                                                       81; Mismatches
                                                                                                                                                                                                                                                         Score 2220; DB 2;
Pred. No. 5.8e-186;
31; Mismatches 198;
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CELLS

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Gaps

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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.025202
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 598
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                        Matches
                                                                                                     Query Match
Best Local Similarity
                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e OTHER INFORMATION: synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP2 (-09-532-594B-16
                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
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                                            TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESVPDPQPLGEPPATPA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTEPRPIGTRYLTRPL 736
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   AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL
                                TAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSG-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRTTRPIGTRYLTRPL
                                                                                       Conservative
                                                                                       45.9%; Score 1830.5; DB 2; 57.8%; Pred. No. 7.2e-152; ative 74; Mismatches 154;
                                                                                        Indels 31;
                                                                                                                 Length 598;
                                                                                        Gaps
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRIFILE AREFERENCE: 14014, 0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT APPLICATION NUMBER: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
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US-09-533-427-5
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                                                                                                            US-09-533-427-5
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                                          Query Match
Best Local Similarity 55.0
Conservative
                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                       OTHER INFORMATION: Description of Artificial OTHER INFORMATION: synthetic construct
                                                                                                                                                                               TYPE: PRT
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  PKRKKARTEEDSKPSTSS
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                                                                  42.6%;
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                                                       64;
                                                     Score 1700.5; DB 2; Pred. No. 1.9e-140; 4; Mismatches 173;
                                                                                                                                        Sequence:/No.
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  -DAEAGPSGSQQLQIPAQPASSL
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APPLICANT: Davidson, Beverly
III'LE OF INVENTION: AAVA VECTOR AND USES THEREOF
FILE REFERENCE: 14014.025202
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
TYPE: PRT
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US-09-532-594B-18
; Sequence 18, Application
; Patent No. 6468524
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                                              Matches
                                                          Query Match
Best Local Similarity
                                                                                                      ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: synthetic construct
NAME/KEY: misc feature
OTHER INFORMATION: AAV4 capsid protein VP3
-09-532-594B-18
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chorini, John A. APPLICANT: Kotin, Robert M. APPLICANT: Safer, Brian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DNVMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDV
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736
                                                          42.4%; Score 1690.5; DB 2; 59.4%; Pred. No. 1.3e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09532594B
                                              65,
                                              Mismatches
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                                              132;
                                                                                                                                                                Sequence; No.
                                            Indels
                                                                       Length
                                                                           544;
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                                              25;
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중 유

ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 322

MSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYREIKS

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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Bafer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAVS VECTOR FOR TRANSDUCING BRAIN CELLS AND LUNG CELLS
FILE REFERENCE: 14014.0323U2
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 532
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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Matches
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Patent No. 6855314
GENERAL INFORMATION:
                                                                                        Query Match
                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:/No. OTHER INFORMATION: synthetic construct
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203 MASGGGAPMADNNBGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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                                                      Conservative
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                                                41.7%; Score 1665; DB 2; 58.9%; Pred. No. 2.1e-137; tive 54; Mismatches 154;
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532	GOVTVEMEWELKKENSKRWNPEIQYTNNYNDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL	473	В
736	GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL	677	Ş
472	PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVSSFITQYST	414	문
676	PIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYST	617	Ş
413	NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEIVPGSVWMERDVYLQG	354	망
616	NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG	557	ş
353	VSAFATTINRMELEGASYQVPPQPNGMTNNLQGSNTYALENTMLFNSQPANPGTTATYLEG	294	В
556	NFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD	500	Ş
293	QYLYRFVSTNNTGGVQFNKNLAGRYANTYKNWFPGPMGRTQGWNLGSGVNRAS	241	DЬ
499	LLFSRGSPAGMSVQP-KNWLPGPCYRQQRVSKTKTDNNNS	441	Q
240	RDNTENPTERSSFECLEYFPSKMLRTGNNFEFTYNFEEVPFHSSFAPSQNLFKLANPLVD	181	DЬ
440		383	Ş
180	EVTVQDSTTTIANNLTSTVQVFTDDDXQLPXVVGNGTEGCLPAFPPQVFTLPQXGYATLN	121	Вb
382	EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN	323	Ş
120	GSVDGSNANAYFGYSTPWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVK 1	61	ఠ

Search completed: November 23, 2005, 17:42:46 Job time : 36.4724 secs



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Post-processing: Minimum
Maximum
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Gapop 10.0 ,
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Copyright (c) 1993 - 2005 Compugen
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AC Q9MBP8;
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Best Local Similarity
Matches 736; Conserv
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Xiao W., Chirmule N., Berta S.C., McCullough B., Ga
Xiao W., Chirmule N., Berta S.C., McCullough B., Ga
Gene therapy vectors based on adeno-associated vir
J. Virol. 73:3994-4003(1999).

EMBL; AF063497; AAD27757.1; -; Genomic_DNA.

SMR; O9WBP8; 217-736.

SMR; O9WBP8; 217-736.

GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 736 AA; 81375 MW; CFABFB9BD5CD0595 CRC
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     GCLPPFPADVFMI PQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
                                    TISTRIWALPTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSPRDWQRL
                                                                                                                TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
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Q6JC62_9VIRU
Q6JBZZ_9VIRU
Q6JC02_9VIRU
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GO; G0:0019028; C:viral capsid; IEA.
GO; G0:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81317 MW; 373C7C40975CD9BD
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530611; AA599296.1; -; Genomic_DNA.
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Viruses; ssDNA viruses;
VCBI_TaxID=272636;
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MEDIINE-98080418; PubMed-9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
Rutledge E.A., Halbert C.L., Russell D.W.;
"Infectious clones and vectors derived from ac
(AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).

EMBL; AF028704; AAB95450.1; -; Genomic_DNA.
SNR; O56137; 217-736.
SNR; O56137; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:001518; F:structural molecule activit
InterPro; IPR001403; Parvo_coat.
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SEQUENCE 736 AA; 81411 MW;
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3; Mismatches 3;
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C7 101, 2004 (TremBLrel. 2:

O5 -JUL-2004 (TremBLrel. 2:

O5 -JUL-2004 (TremBLrel. 2:

O5 -JUL-2004 (TremBLrel. 2:

Capsid protein VP1.

Name=cap;

Name=cap;

Adeno-associated virus.

Viruses; ssDNA viruses; P.

NCBI TaxID=272636;

[1]
Gao G., Vandenberghe L.H., Al-
Wilson J.M.;
"Clades of Adeno-associated v
tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AY530606; AAS99291.1; -
SMR; QGJCl3; 218-737.
GO; GO:0019028; C:viral capsi
                                                             NUCLEOTIDE SEQUENCE.

PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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O6JC12 9VIRU PRELIMINARY;
O6JC12;
O6JC12;
O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
O5-JUL-2004 (TrEMBLrel. 2
Adeno-associated virus.
Viruses; ssDNA viruses;
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J. Virol. 78:6381-6388(2004).

EMBL; AY530607; AAS99292.1; -; Genomic_DNA.

SMR; Q6C012; 217-736.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; PARVO Coat; 1.

SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CRC64;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004; Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
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             YTEPRPIGTRYLTRPL
                                                                                                            MIFGKESAGASNTALDNVMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMG
                                                                                                                                                 GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGV
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                                                                       ALPGMVWQGRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPA
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RESULT 6
QGJC10 9VIRU
QGJC10 9VIRU
ID QGJC10;
AC QGJC10;
AC QGJC10;
DT 05-JUL-2004 (TrEMBLrel. 2:
DE Capsid protein VP1.
GN Name=cap;
OS Adeno-associated viruses; Pace of Viruses; RSDNA viruses; Pace of Viruse
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Best Local Similarity
Matches 711; Conserv
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J. Virol. 78:6381-6388(2004).
EMBL; AX530609; AAS99294.1; -; Genomic_DNA.
SMR; Q6JC10; 217-736.
G0; G0:00019028; C:viral capsid; IEA.
G0; G0:00019028; F:structural molecule activity; II
InterPro; IPROUT403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81388 MW; BA9463E970028DF0 CI
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                                                                      GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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Pred. No. 7.3e-241;
9; Mismatches 16;
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Query Match
Best Local Similarity
Matches 640; Conserv
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01-JUN-1998 (TrEMBLrel. (
01-JUN-1998 (TrEMBLrel. (
01-MAR-2004 (TrEMBLrel. (
Capsid protein VP1
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MEDLINE-98080418; PubMed=9420229;
"Infectious clones and vectors derived from adeno-associated virus (AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).
EMBL; AF028705; AAB95452.1; -; Genomic_DNA.
SMR; O56139; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:structural molecule activity; IEA.
InterPro; IPR001403; Parvo_coat.
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19_9VIRU
O56139_9VIRU PRELIMINARY;
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NCE 736 AA;
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                                                                                               GCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVP
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                                                                     GCLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYTFEDVP
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AA; 81906 MW; DD52331AD5F0D70F CRC64;
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Pred. No. 1e-218;
B; Mismatches 57;
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Best Local (
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EMBL; U49704; AAC55049.1; -; Genomic_DNA
SMR; Q65311; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ac
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 736 AA; 81660 MW; AFF1EF47B
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Q65311;
Q1:00-1996 (TrembLrel. 01,
01-NOV-1996 (TrembLrel. 01,
01-NOV-1996 (TrembLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96266430; PubMed-8661429; DOI=10.1006/viro.1996.0367; Muramatsu S., Mizukami H., Young N.S., Brown K.E.; "Nucleotide sequencing and generation of an infectious clone associated virus 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssDNA viruses;
NCBI_TaxID=46350;
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Adeno-associated virus 3.
--^^\ viruses; Parvoviridae;
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                                   TTSTRTWALPTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
                                                                                                    SVPDPQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVI
                                                                                                                          SVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVI
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         TTSTRTWALPTYNNHLYKQISSQS-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRL
                                                                                                                                                                                          AKKRILEPLGLVEBAAKTAPGKKGAVDQSPQEPDSSSGVGKSGKQPARKRLNFGQTGDSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.6%; Score 3494; DB 2;
86.4%; Pred. No. 1.3e-217;
tive 39; Mismatches 59;
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O808Y3 9VIRU PRELIMINARY,
O808Y3;
O1-JUN-2003 (Tremblrel, 2
O1-JUN-2003 (Tremblrel, 2
O1-JUN-2004 (Tremblrel, 2
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MEDLINE=22631657; PubMed=12716974; DOI=10.1073/pnas.0937739100;

Gao G., Alvira M.R., Somanathan S., Lu Y., Vandenberghe L.H.,

Rux J.J., Calcedo R., Sanmiguel J., Abbas Z., Wilson J.M.;

"Adeno-associated viruses undergo substantial evolution in prime
during natural infections.";

Proc. Natl. Acad. Sci. U.S.A. 100:6081-6086(2003).

Proc. Natl. Acad. Sci. U.S.A. 100:6081-6086(2003).

SMR, O80873; 217-736.

SMR, O80873; 217-736.

GO; GO:0019088; C:viral capsid; IEA.

GO; GO:0019089; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-human primate Adeno-associated virus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae;
NCBI TaxID=226582;
[1]
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Name=VP1;
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SEQUENCE 736
                                                                                                                                                                                                                                                                                                                                interPro;
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G0:0005198; F:structural molecule activity;
erpro; IPR001403; Parvo_coat.
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  KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ
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AA; 81370 MW;
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Pred. No. 3e-216;
4; Mismatches 6
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Query Match
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Chen C.L., Jensen R.L., Schnepp B.C., Connell M.J., Bart Chen C.L., Shell R., Johnson P.R., Clark K.R.;
Sferra T.J., Shell R., Johnson P.R., Clark K.R.;
"Characterization of Adeno-Associated Viruses In Childre Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases EMBL; AY695376; AAU05370.1; -; Genomic_DNA.
SMR; Q670Q8; 217-735.
                                                                                                                                                                                                                                                                                                                                                      Adeno-associated virus. Viruses; ssDNA viruses; NCBI_TaxID=272636;
                                            GO; GO:0019028; C:viral capsid; GO; GO:0005198; F:structural mol InterPro; IPR001403; Parvo_coat. Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81887 MW; 2
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  NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
Wilson J.M.;
                                                            Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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"Clades of Adeno-associated viruses are widely disseminated tissues.";
J. Virol. 78:6381-6388(2004).
EMBL; AYS30622; AAS99307.1; -; Genomic_DNA.
SMR; Q6GBZ7; 217-735.
G0; G0:0019028; C:Viral capsid; IEA.
G0; G0:0005198; F:Structural molecule activity; IEA.
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A CRC64;
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84.5%; Pred. No. 3.5e-215;
tive 49; Mismatches 64;
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EMBL; AY530567; AAS99252.1; -; Genomic_DNA.

SMR; QGJC52; 218-737.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity;

InterPro; IPR001403; Parvo_coat.

Pfam; pF00740; Parvo_coat; 1.

SEQUENCE 737 AA; 81538 MW; CC68EB97BE11F25C
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Viruses; ssDNA viruses;
NCBI TaxID=272636;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PabMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PabMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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 PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDETVDN
                                                          NQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPAN
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05-JUL-2004 (TrEMBLrel. 2
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                                                        PFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNAGGTAGNRELQFYQGGPTTMAEQAKNW
                                                                           PFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQ-NQSGSAQNKDLLFSRGSPAGMSVQPKNW
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PPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNFDKQTGVDFAVDS 737

NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Paddenderghe L.H., Alvira M.R., Lu Y., Calcedo of Adeno-associated viruses are widely Parvoviridae; Created) Last seq Last ann sequence up annotation Parvovirinae; 737 update) ₹ update) disseminated Dependovirus ₽ ; Zhou in human

SMR; Q6JC58; 218-737.
GO; GO:0019028; C:viral capsid; IE
GO; GO:0005198; F:structural molec
InterPro; IPR001403; Parvo\_coat.
Pfam; PF00740; Parvo\_coat; 1.
SEQUENCE 737 AA; 81486 MW; EF6 J. Virol. 78:6381-6388(2004).
EMBL; AX530561; AAS99246.1; -;
SMR; \_\_GGJC58; 218-717 48; Score 3455.5; DB 2 Pred. No. 4.1e-215; 48; Mismatches 55; molecule Genomic\_DNA EF6B85A99F0F7CB5 IEA. activity; DB 2; CRC64; IEA Length ω • Gaps

1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD ESVPDPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNKGADGVGNASGNWHCDSTWLGDRV AKKRVLEPLGLVEBAAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS AKKRVLEPLGI.VEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS ITTSTRTWALFTYNNHLYKQISSASTGASNDNHYFGYSTFWGYFDFNRFHCHFSFRDWQR ESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRV MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD ITTSTRTWALFTYNNHLYKQISSQSAGSTNDNVYFGYSTFWGYFDFNRFHCHFSPRDWQR 120 359 300 299 240 239 180 179 120 60

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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Calcedo
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Viruses; ssDNA viruses;
VBI_TaxID=272636;
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J. Virol. 78:6381-6388(2004).
EMBL; AY530591; AAS99276.1; -;
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05-JUL-2004 (TrEMBLrel. 2:
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecul
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 738 AA; 81582 MW; 585F4
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EMBL; AY530600; AAS99285.1; -;
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Viruses; ssDNA viruses;
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       AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS
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48; Mismatches
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Search completed: November 23, 2005, 17:41:16 Job time : 144.766 secs

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probable transketo	T52289	N	739	3.0	118	تن
toxin-like outer m	H71879	N	2399	3.0	118.5	N
transcription fact	A41311	N	667	3.0	119	μ
probable membrane	AC0314	N	2004	3.0	119.5	0
IgA-specific serin	S60762	N	1394	3.0	119.5	9
hypothetical prote	E86719	N	1180	3.0	119.5	8
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toxin-like outer m	B64635	N	2529	3.1	123.5	μ
probable TonB-depe	AB0124	N	690	3.1	123.5	0

## ALIGNMENTS

coat protein - adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 09-Jul-2004
C;Accession: A03698
R;Srivastava, A.; Lusby, E.W.; Berns, K.I.
J. Virol. 45, 555-564, 1983
A;Title: Nucleotide sequence and organization of the adeno-associated virus 2 genome.
A;Reference number: A03694; MUID:83164299; PMID:6300419
A;Accession: A03698
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-504 <SRI>A;Residues: 1-504 <SRI
A;Residues: 1-504 <SRI Local Similarity 383 NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG BEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAKI WTGATKYHLNGRDSLVNP--AMASHKDDEEKFFPQSGVLIFGKQGSEKTNVNIEKVMITD WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD LYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY EEEIGTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKI Conservative 54.6%; Score 2177.5; DB 1; 82.5%; Pred. No. 3.9e-134; ive 33; Mismatches 47; Indels Length 504; ω •• Gaps 622 562 299 502 442 179 382 119 322 60 357 239

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A;Molecule type: DNA
A;Residues: 1-732 <ZAD>
A;Residues: 1-732 <ZAD>
A;Residues: 1-732 <ZAD>
A;Cross-references: UNIPROT:Q83289; UNIPARC:UPI00000F6CSD; EMBL:X75093; NID:g609091;
A;Experimental source: strain FM
C;Genetics:
C;Genetics: VP1
C;Guperfamily: parvovirus coat protein
C;Keywords: coat protein
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R;Zadori, Z.; Erdei, J.; Nagy, J.; Kisari, J.
submitted to the EMBL Data Library, September 1993
A;Reference number: S52209
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N;Alternate names: VP1 protein
C;Species: muscovy duck parvovirus
C;Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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LKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEV
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                                                         TVTINEQNTTAPTINAELEVLGALPGMVWQNRDIYLQGPIWAKIPKTDGKPHPSPNLGGFG
                                                                                       VAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFG
                                                                                                                              PVATTHIEDQASSVPAQNIIGIAKDPYRSGSTLAGISDIMVTDEQEIAPTNGVGWRPYGL
                                                                                                                                                                TAMASHKDDEDKFFPMSGVMIFGKE--SAGASNTALDNVMITDEEEIKATNPVATERFGT
                                                                                                                                                                                                                                       SRGSPAGMSVQPKNWLPGPCYRQQRVSKTK--TDNNNSNFTWTGASKYNLNGRESIINPG
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                                                                                                                                                                                                       KKAVKGAFGAMGRNWLPGPKLLDQRVRAYSGGTDNYANWSIWSKGNKVFLKDREYLLQPG
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Pred. No. 2.6
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A;Title: Complete nucleotide sequence and genome organization A;Reference number: A26104; MUID:87061184; PMID:3783814
A;Recession: A26104
A;Accession: A26104
A;Residues: 1-673 < CHE>
A;Residues: 1-673 < CHE>
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
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N;Contains: coat protein VP2

C;Species: bovine parvovirus

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Ju1-2004

C;Accession: A26104
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     TFTREARTKLITGSNGADGDYKEWWMLPNQMWDSAPISRYNPIWVKVPRVNRKTLLDTQD
                                       REGIVAVNEOSSSIDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHIDGHEHPSPLM
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                                                                                                                                                                                    GPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGV
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                                                                            RAVRVGYSTDPİYGGQQPESDLLRLRYSASAAEGQQNPILEN--
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Pred. No. 3.7e-44;
                                                                                                              -----SAGASNTALDNVMITDEEEIKATNPVATE
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A;Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; C;Superfamily: parvovirus coat protein C;Keywords: coat protein
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A;Title: Nucleotide sequence and genome organization of A;Reference number: A24299; MUID:86200451; PMID:3701931
A;Accession: A24299
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C;Species: parvovirus B19
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A2429
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A; Residues: 1-781 <SHA>
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Best Local Similarity
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| WRPEYMHS---ATIMSVDAYTINNAGVY
                                                                                                                                                                                                                                                                                                                                                                                                        NNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNN-GSQAVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSASTGASND------NHYFGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTGQQP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĠSIPMSHPPGTIFIKLARIPVPGNGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVT--TNDGVTTIA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MWSEGATFSANSVTCTFSRQFLIPYDPEHHYKVFSPAASSCHNASGKEAKVCTISPIMGY
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PIWAKIPHTDGHFHPS-PLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYS
                                                                                                                                                              GASKYNLNGRESIINPG-TAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNV-----
                                                                                                                                                                                                                                               YLNRTONOSGSAONKDLLFSRGSPAGMSVOPKNWLPGPCYROORVSKTKTDNNNSNFTWT
                                                                                                                                                                                                                                                                                           KLASEESAFYVLEHSSFQLLGTGGTASMSYKFPPVPPENLEGCSQHFYEMYNPL---YGS
                                                                                                                                                                                                                                                                                                                                                                          DSTTGRLCMLVDHEYKYPYVLGQGQDTLAPELPIWVYFPPQYAYLTVGDVNTQGISGDSK 429
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                                                                                                                      GLSTGTSQNTRISLRPGPVSQPYHHWDTDKYVTGINAISHGQTTYG---NAEDKEYQQGV
                                                                                                                                                                                                            RLGVPDTLGGDPKFRSL-----THEDHAIQPQNFMPGPLVNSVSTKEGDSSNTGAGKALT
                                                                                                                                                                                                                                                                                                                                ----RSSFYCLEYFPSOMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQYLY
                                                                               --MITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
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                                       ---FPNKGTQQYTDQIE-RPLMVGSVWNRRALHYES
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A60006
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C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Nucleotide sequence of capsid protein gene of porcine A;Reference number: A60006; MUID:89319168; PMID:2750278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, Virus Res. 13, 79-86, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: porcine parvovirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A60006
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A; Residues: 1-729 <SAK>
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                                           QYNDDE----PNGAIRFTMGYQHGQLTTS----SQELERYTFNPQSKCGRAPKQQFNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMA 212
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                                                                                     SHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITDEEEIKATNP-----VATERFGT 579
                                                                                                                                                                    PAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP--GTAMA
                                                                                                                                                                                                                                                       EVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNKDLLFSRGS
                                                                                                                                                                                                                                                                                             YLSCTRNLNPPTYTGQSQQITDSIQTGLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFD
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                                                                                                                                                                                                              TKPL--KLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTMNNSYTEAT
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                                                                                                                             -----AQVGYNTPYMNFEYSNGGPF-----LTPIVPTADT
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A;Molecule type: DNA
A;Residues: 11-729 <BER>
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Ju1-2004
C;Accession: B33743; D48472
R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.
Virology 173, 368-377, 1989
A;Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal
A;Reference number: A33743; MUID:90085785; PMID:2596019
A;Accession: B33743
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C;Superfamily: parvovirus coat protein
C;Keywords: coat protein; glycoprotein
C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate
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Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and
A;Reference number: A48472; MUID:94025614; PMID:8212598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P18546; UNIPARC:UPI0000127C70; GB:M32787; NID:g332983; R;Bergeron, J.; Menezes, J.; Tijssen, P.
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A; Residues: 1-729 < VAS>
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                                                                                                             GVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVL
                                                                                                                                                   GAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQV
                                                                                                                                                                                                                           DNNEGADGVGNASG--NWHCDSTWLGD---RVITTSTRTWALPTYNNHLYKQIS--SAST
                                                                                                                                                                                                                                                                 PAPRHIFINLAKKKAKGTSNTNSNSMSENVEQHNPINAGTEL-SATGNESGGGGGGG---
                                                                                                                                                                                                                                                                                                                                         ETEHAKDYGGKIGHYFFRAKRAFAPKL---SETDSPTTSQQPEVRRSPRKHPGSKPPGKR
                                                                                                                                                                                                                                                                                                                                                                             RLQEDTSFGGNLGRAVFQAKKRVLBPLGLVEEGAKTAPGKKRPVEQSPQBPDSSSGIGK-
                                                                                                                                                                                                                                                                                                                                                                                                                  RGLTLPGYKYLGPGNSLDQGEPTNPSDAAAKBHDEAYDKYIKSGKNPYFYFSAADEKFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQE
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                                                                                                                                                                                        -GGRGAGGVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSES
                                                                                                                                                                                                                                                                                                    ----TGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMA
                                   KTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRY
                                                                        KEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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-TLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF-TFSYTFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 482; DB 1; 25.5%; Pred. No. 1.7e-23; tive 111; Mismatches 310
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Best Local
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J. Virol. 55, 574-587, 1985

A;Tille: Cloning and sequence of DNA encoding structural A;Reference number: A03697; MUID:85265017; PMID:2991581 A;Accession: A03701
A;Molecula to the control of the contro
A;Molecule type: DNA
A;Residues: 1-727 <CAR>
A;Kesidues: 1-727 <CAR>
A;Cose references: UNIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:g333474; PID:
C;Genetics: 11/1
C;Genetics: 11/1
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coat protein VPI - feline panleukopenia virus N;Contains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 30-Jun-1987 #sequence_revision 30-Jun-C;Accession: A03701 R;Carlson, J.; Rushlow, K.; Maxwell, I.; Maxwe
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30-Jun-1987 #text_change 09-Jul-2004
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coat protein VPI - mink enteritis virus (strain Abashiri)
N;Contains: coat protein VP2
C;Species: mink enteritis virus, MEV
C;Species: mink enteritis virus, MEV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B38350
R;Kariatsumari, T.; Horiuchi, M.; Hama, E.; Yaguchi, K.; Ishigurio, N.; Goto, H.;
J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone A;Reference number: A38350; MUID:91202123; PMID:2016597
A;Accession: B38350
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VCPVME
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A;Residues: 1-722 <KAR>
A;Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
A;Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;139-722/Product: coat protein VP2 #status predicted <VP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DVFMIPQYGYLTLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF-TFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRYY
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                                                                                                                                                                                                                                                                                                                       GLVLPGYKYLGPFNGLDKGEFVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQER 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTEPRPIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPVTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-----PVYPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDPRYAFGRQHGQKTTTTGETPERFTYIAHQDT-------GRYPAGDWIQNINF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQWDRTLIPSH-----TGTSGTPTNIYHGTDPDDVQFYTIENSVPVHLLRTGDEFATGT
                                                                                                                                                                          TKDATDWGGKIGHYFFRAKKAIAPVLTDTPDNPSTSRPTK-PTKRSKPPPHIFINLAK--
                                                                                                                                                                                                                          LQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YL-PNNIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFSATKFASFITOYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGL
ADGVGNASGNWH---
                                                                                                              QQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAAVGPTTMASGGGAPMADNNEG 217
                                                                                                                                                                                                                                                                                      GLVPPGYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYFSPADQRFIDQ
                                                     ----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 439.5; DB 1; ilarity 23.6%; Pred. No. 9.6e-21; Conservative 117; Mismatches 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728
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     -CDSTWLGDRVITTSTRTWALPTYNNHLYKQI--
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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     -SSA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                               coat protein VPI - feline panleukopenia virus (strain 193)
N;Contains: coat protein VP2
C;Species: feline panleukopenia virus, FPLV
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B36608
C;Accession: B36608
R;Martyn, J.C.; Davidson, B.E.; Studdert, M.J.
J. Gen. Virol. 71, 2747-2753, 1990
A;Title: Nucleotide sequence of feline panleukopenia virus: comparison with canine;
A;Reference number: A36608; MUID:91073139; PMID:2174965
A;Accession: B36608
A;Molecule type: DNA
A;Residues: 1-727 <MARN
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                                                                                                                                                                                                                                                                                                                       C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
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  103 RLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGKT : |: | : | | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 TEPRPIG 728
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                                                                                      h 10.8%;
Similarity 23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN----
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                                                                                                                                                                                                           Conservative 117;
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                                                                                                                                                                                                                                      Score 431.5; DB 1
Pred. No. 3.2e-20;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                    DB 1;
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RESULT 10
VCPVPP
VCPVPP
Coat protein VP1 - porcine parvovirus
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Species: porcine parvovirus
C;Accession: B33302
C;Accession: B33302
C;Accession: B3302
C;Accession: B3302
A;Renz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A;Title: Porcine parvovirus: DNA sequence and genome organization.
A;Accession: B33302
A,MCleonia B3302
A,MCleonia B3302
A,MCleonia B3302
                                                                                                                      A; Cross-references:
C; Genetics:
                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-723 < RAN>
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                                                                                                 A; Introns: 10/1
                                       ;145-723/Product:
                                                          ;Superfamily: parvovirus coat protein
;Keywords: coat protein
                                                                                                                    Genetics:
  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YV-PNNIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GASKY---NLNGRESIINPGT----AMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTTEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- DVFMIPQYGYLTLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF-TFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKGNMALDDIHVQIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALPTYNNHLYKQI-----SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTEPRPIG 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAGRGGAQTDENQAA----D
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                                     coat protein VP2 #status predicted <VP2>
                                                                                                                                        UNIPROT: P18546; UNIPARC: UPI0000174964; EMBL: D00623
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10.7%;
  Score
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  426;
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Length 723;
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                                                                                                                       621
                                                                                                                                                       628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSESGSAGQMVQD
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                                     TAKMRSSNMWNPIQQHTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQAIFNVVLKTITESATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNASGNWH--CDSTWLGD---RVITTSTRTWALPTYNNHLYKQI-----S8ASTGAS-ND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGPGNSLDQGEPTNPSDAAAKEHDEAYDKYIKSGKNPTFYFSAADEKFIKETEHAKDYGG
                                                                                                                                                                                                                                                                                                                                                                 NWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINP--GTAMASHKDDEDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPTYTGQSQPNNRLNTNRLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPL--KLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRYYLSCIRNLN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKKAKGTSNTNSNSMSENVEOHNPIN--AATELSATGNESGGGGGG----GGRGAGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGG 112
                                                                                    ELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                     RLH---VTAPFVCKNNPPGQLFVKIAP---NLTDDFNADSPQQPRIITYSNFWWKGTLTF
                                                                                                                                                       HFHPSPLMGGFGLK-NPPPQILIKNTPVPANPPAEFSA-TKFASFITQYSTGQVSVEIEW
                                                                                                                                                                                           NLENTINGTLLPSDPIGGKSNMHFMNTLNTYGPLTALNNTAPVFPNGQIWDKELDTDLKP
                                                                                                                                                                                                                        NFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDVYLQGPIWAKIPHTD--G
                                                                                                                                                                                                                                                                                           FPMSGVMIFGKESAGASNTALD---NVMITDEEEIK--ATNP-----VATERFGTVA-V
                                                                                                                                                                                                                                                                                                                                                                                                   HSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTINNSYTEAT----AIRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --TLNNGSQAVGRSS------FYCLE-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                               AQVGYNTPYMNFEYSNGGPF-----LTPIVPTADTQYNDDEPN-
                                                                                                                                                                                                                                                            -GAIRFTMDYQHGHLTTSSQELERYTFNPQSKCGRAPKQQFNQQAPL
                                                    TAENIGKYI-PTNIG
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A;Accession: B23008
A;Molecule type: DNA
A;Residues: 1-718 <SAH>
A;Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963;
R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. 57, 656-669, 1986 EMBL: X02481; variants of. NID: 960918; the autonomous

#text\_change

09-Jul-2004

A;Title:

DNA sequence of the lymphotropic variant of minute virus of

mice, MVM(i),

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PIDN

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A;Reference number: A29510; MUID:86115415; A;Accession: B29510
A;Molecule type: DNA
A;Residues: 1-143; A;145-718 <AST>
A;Cross-references: UNIPARC:UPI0000127D6C; C;Superfamily: parvovirus coat protein C;Keywords: coat protein
RESULT 12
VCPVCP
Coat protein VP1 - canine parvovirus (strain N;Contains: coat protein VP2
C;Species: canine parvovirus, CPV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun C;Accession: B29962
R;Reed, A.P.; Jones, E.V.; Miller, T.J.
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                                                                                                                                       SRIVTYGTFFWKGKLTMRAKLRA----NTTWNPVYQ-
                                                                                                                                                                                        SPVYPQGQIWDKELDLEHKPRLHITAPFV---CKNNAPGQMLVRLGPNLTDQYDPNGATL
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J. Virol. 62, 266-276, 1988
A;Title: Nucleotide sequence and genome organization of canine A;Reference number: A29962; MUID:88062992; PMID:2824850
A;Accession: B29962
A;Accession: B29962
A;Molecule type: DNA
A;Residues: 1-748 <REE>
A;Cross-references: UNIPROT:P12930; UNIPARC:UPI0000127D7B; EMBL
C;Genetics:
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C; Superfamily: parvovirus
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                                                                            TPVPAN----PPAEFSATKFASFITQYSTGQVSVEIEWELQKEN9KRWNPEVQYTSNYAKS
                                                                                                                                                                                                         YPEGDWIQNINFNLPVTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-
                                                                                                                                                                                                                                                                                               PIAAGRGGAQTYENQAADGDPRY---
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ANVDETVDNNGLYTEPRPIG
                                         APNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN----
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C;Superfamily: parv
C;Keywords: coat p:
F;584-737/Product:
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                                                                                                                                                                          ----GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD------
                                                                                                                                                                                                                                               MSVQPKNWLPGPCYRQQRVSKTKTDNNNSNF-----TWTGASKYNLNGRESIINP-
                                                                                                                                                                                                                                                                                                                SYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAG
                                                                                                                                                                                                                                                                                                                                                                                     ---- DVFMIPQYGYLTLNNGSQAVGRS-----SFYCLE-YFPSQMLRTGNNF-TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVNGNMALDDIHAQIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSGGVGISTGTFNNQTEFKFLENGWV--EITANSSRLVHLNMPESENYRRVVVNNMDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQEPDSSSGIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEGKDLITYKYLGPGNSLDQGEPTNPSDAAAKEHDEAYAAYLRSGKNPYLYFSPADQRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQ 101
                                                                                                                                                                                                                                                                                TFFFDCKP--CRLTHTWQTNRALGLPP-----FLNSLPQSEGATNFGDI------
                                                                                                                                                                                                                                                                                                                                                   YFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDDVQFYTIENSVPVHLLRTGDBFATG
                                                                                                                                                                                                                                                                                                                                                                                                                      KTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGADGVGNASGNWH------CDSTWLGDRVITTSTRTWALPTYNNHLYKQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERATGSGNGSGGGG------G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQTKDAKDWGGKIGHYFFRAKKAIAPVLTDTPDHPSTSRPTK-PTKRSKPPPHIFINLAK 137
                                RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------NPPPQILIKNTPVPA
                                                                    WIQNINFNLPYTNDNVLLPTDPIG----GKTGINY--TNIFNTYGPLTALNNVP-----
                                                                                                                                        KTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPERFTYIAHQDTGRYPEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCL-----PPFPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGQQPAKKRLNFGQTGDSESVP----DPQPLGEPPA--TPAAVGPTTMASGGGAPMADNN
 - PVYPNGQIWDKEFDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 407.5; DB 1; ilarity 22.8%; Pred. No. 1.2e-18; Conservative 112; Mismatches 301;
                                                                                                     --- NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coat protein VP2 #status predicted
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PMID:3176341
 LKPRLHVNAPFVCQNNCPGQLFVKVAPNLT
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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_ch
C;Accession: A03699
R;Rhode III, S.L.; Paradiso, P.R.
U. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and
A;Reference number: A03695; MUID:83112183; PMID:6823009
A;Accession: A03699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-722 <RHO>
A;Cross-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D; EMBL:X01457; EMBL:J02198
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 NGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KKRLNFGQTGDSESVPDPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGN 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFFRTKRAFAPKLSTDSE----PG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N---PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDF 713
                                                                                                                                                                                                                                                                                                                  QGAGQDAIKVYNNDLTACMMVALDSNNILPYTPAAQTSETLGFYPWKPTAPAPYRYYFFM
                                                                                                                                                                                                                                                                                                                                                                                                                    SNDNHYFGYSTPWGYFDFNREHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTT- 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASGNWHCDSTW--LGDRVITTSTRTWAL------PTYNNHLYKQISSASTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARAKKKRASLAAQQRTLTMSDGTETNQPDTGIANARVERSADGGGS-SGGGGGGGGGGG 171
ITDEEEIKA-TNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPI
                                  GKQHGEDWAKQGAAPERYTWDAIDSAAGRDTARCFV-----
                                                                      NGR--ESIINPGTA------MASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVM
                                                                                                                                                                          LKLTHTWQTNRHLACLQGITDLPTSDTATASLTANGDRFGSTQTQNVNYVTEALRTRPAQ
                                                                                                                                                                                                             FHSSYA----HSQSLDRLMN-PLIDQYLYYLNRTQNQSGSAQNKDLLF------
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                                                                                                         IGFMOPHDNFEANRGGPFKVPVVP
                                                                                                                                        -----SRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNL
                                                                                                                                                                                                                                               PRQLSVTSSNSAEGTQITDTIGEPQALNSQFFTIENTLPITLLRTGDEFTTGTYIFNTDP
                                                                                                                                                                                                                                                                                PQYGYLTLNNGSQ-----AVG-----RSSFYCLE-YFPSQMLRTGNNFTF-SYTFEEVP
                                                                                                                                                                                                                                                                                                                                                   ----NDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCL-----PPFPAD---VFMI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 404; DB 1
Pred. No. 2e-18;
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                                                                                                           ----LDITAGEDHDAN----
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-QSAPISIPPNQNQI

618 563 GAIRFNY

513

511

290

231 267

410

420 350

619 MAKIPHTDGHFHPSENGFGLKNSPEPHDD. 619 MAKIPHTDGHFHPSENGGFGLKNSPEPHDE. 614 WAKIPHTDGHFHPSENGGFGLKNSPEPHDE. 614 WAKIPHTDGHFHPSENGGFGLKNSPEPHDE. 615 WAKIPHTDGHFHPSENGGFGLKNSPEPHDE. 616 WAKIPHTDGHFHPSENGKALRENLTWTAPFVKRNPPGGLFWHLGPNLTDGFDENSTTVSRIVT- 617 YSTGYVSVELENELKKNSKENNERVYYGATTD 687 618: Cast protein V2 619 YSTGYVSVELENELKKNSKENNERVYYGATTD 687 619 YSTGYVSVELENELKKNSKENNERVYYGATTD 687 610: AGAINE PARTVOVITUS (strain 780929) 610: AGA 630-633, 1985 6111, S.L. 6113, S.L. 6114, 630-633, 1985 6115, S.L. 6115, S.L. 6115, S.L. 6116, S.L. 6117, S.L	ફ	유 성	유 상	유 왕	8 8	유 성	유 성	B 8	용 성	Quer Best Matc	A;Mol A;Res A;Cro C;Gen C;Gen C;Sup C;Sup F;139	J. Vi J. Vi A;Tit	RESULT VCPVCN coat p COat p N;Cont C;Spec C;Date C;Acce	8 8	B &	8
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THMMYNNVĖNSYGPLSAFPHPDD	25.5	SYAH  -	YGYL	TKVY	YFGY ; HAQI	NWH- :: TENN	FGQT  - AGQV	NLGR :  KIGH	LGPFI 	arit; onse	NA <rho : UN : UN rote coal</rho 	633, e ser e AO:	can rote parvo 7 #se	QVSVI YWKG:	I PI	SAIAC
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PANPPAEF SATKFASFITQ (		drtb i	GRS-	VFSD      VALD	NRFH   : NAWD	TWLG	DP	LEPL	NAAD   :  NPSD	; S ; P 118;		: 85	virus PV evisi	NSKRI :   PNLTI	PLMGC	:
PANPPAEF SATKFASFITQ (		QYLY!  -  PFLN:	YHGTI	SEYQI	CHFSE  :  VWFNE	DRVII -EIT <i>I</i>	QPLGE     - QPLGE	TATAI :	NAALE 	core	UNIF	COA 856	(st	NPEV  -	FGLK	GPLS
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	TGDT		ENSV	GCL-	NWGF!	TYNNI : MPES!	VGPT    TGSGI	RPVE(	KAGDI ::  RSGKI	B 1; 17; 297;	0017,	gene	##		NTPVE	
, ,		GSAQN 	THAA   :     SQWI		RPKRI	HLYKÇ EKDRR	IMASG :   NGSGG	OSPQE :  RSKPP	NPYLR	Len Ind	966 < VP	E C			ANPP.	
, w		KKKRG	RTGN	dird)	NFKL	NAAA)	GGAP	PDSS.	YNHA ::   FSPA		v EMB	anin	hange		AEF	
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•		460 465	419 409	371 355	325 295	268 235	222 177	168 123	108	35;					573	603

B &	B 64	g Q	Db Qy	gb Qy
727 704	667 659	623 612	563 565	510 518
727 IG 728    704 IG 705	667 FASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRP 726	623 PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATK 666	563 EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI 622	510NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITD 562 
	26 03	58	22	62

Search completed: November 23, 2005, 17:44:00 Job time : 29.9904 secs

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                                                                                           A Geneseq 21:*
1: geneseqp1980;
2: geneseqp1990;
3: geneseqp2000;
4: geneseqp2001
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3251
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                                                                                                                                                                                                                                                                                                                                                                                            2443163 seqs, 439378781 residues
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                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
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geneseqp2001s:*
geneseqp2002s:*
                geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and capsid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of a

Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.

N-PSDB; AAD00772, AAD00778. WPI; 2000-376571/32. Wilson JM,

Xiao W;

Claim 7; Page 93-95; 108pp; English.

7006 Adeno-ass	A0227006	ADZ27006	۰	735	85.8	2789.5	5
	AQZ 2 / 033	ADZ27035	9	735	86.0	2796.5	4
	AGZ2/036	ADZ27036	ø	734	86.1	2798	ü
	Adz2/03/	ADZ27037	9	734	86.1	2800	2
	Adz26999	ADZ26999	9	735	86.2	2802.5	μ
-	AGZ27004	ADZ27004	9	735	•	2803.5	ō
	Adz26994	ADZ26994	9	735	86.2	2803.5	ő
	Adz26998	ADZ26998	9	735	86.4	2807.5	8
-	Adz27003	ADZ27003	9	735	86.4	2807.5	37
	Adz26991	ADZ26991	ø	735	86.4	2808.5	6
	Adz27002	ADZ27002	9	735	86.5	2811.5	5
_	Adz27067	ADZ27067	9	736	86.6	2815	4
_	Adv67507	ADV67507	9	736	86.6	2815	ũ
	Ade7657	ADE76572	7	736	86.6	2815	2
_	Abr62763	ABR62763	7	736	86.6	2815	F
_	Abb8023	ABB80233	σ	736	86.6	2815	5
	Aabby845	AAB59845	4	736		2815	ő
	AGZ2699	ADZ26992	ø	735	86.6	2815.5	æ
9 40	Adz27034	ADZ27034	9	735	86.7	2818.5	7
_	Adz27000	ADZ27000	9	735	86.7	2818.5	26
	AU227070	ADZ27076	¥	735	86.7	2818.5	ŭ

## ALIGNMENTS

## RRSULT 1 RACYLIT 1 RACYLIT 2 RACYLL 2 Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; VP2. 08-SEP-2000 (first entry) AAY71168 standard; protein; 599 AA. WO200028061-A2. AAY71168; 05-NOV-1998; 02-NOV-1999; Adeno-associated virus 1. Adeno-associated virus serotype 1 capsid protein VP2 18-MAY-2000. (UYPE-) UNIV PENNSYLVANIA. 98US-0107114P 99WO-US025694.

for

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                          02-NOV-1999;
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DB; AAD00772, AAD00777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              YLTINNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRIMNP YLTINNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRIMNP YLTINNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRIMNP
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                              IWAKIPHTDGHFHDSPLMGGFGLKNPPBQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                                                                                                                                           VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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                                                                      IWAKI PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in ABB80231-34 represent vpl proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three proteins vpl, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated adeno-associated virus (AAV) comprising an AAV9 useful for preparing a medicament for delivering a transgene
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05-JUN-2002; 2002US-0386132P
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LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
                                              NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG
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Pred. No. 1.4e-253;
Mismatches 0;
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ABR62762 standard;
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                                                                                       QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                                                                 IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
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protein;
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S 片 Ś 밁 Ş 밁 Ş

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Adeno associated virus 1 capsid protein vpl
                                                                                                                                       ABR62762;
Adeno associated
                              AAV; AAV1; capsid;
                                                                                                     (first
   virus.
                                   vector;
                                                                                                     entry)
                                   gene therapy; antisense therapy; vaccine.
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17-DEC-2001; 01-MAY-2002; 05-JUN-2002; 12-NOV-2002; 2002WO-US033630 26-JUN-2003. 2001US-0341151P. 2002US-0377133P. 2002US-0386122P.

Gao G,

(UYPE-)

VIND

PENNSYLVANIA

New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.

Disclosure; Fig 2A-C; 82pp; English.

ARRESULT 4
The present sequence is the protein sequence of the vpl capsid protein of adeno associated virus serotype 1 (AAVI). The invention provides the nucleic acid and amino acid sequences of novel AAV8 and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cells. Among the desirable fragments are the cap proteins, including vpl, vp2, vp3 and hypervariable regions, the rep proteins, including rep78, rep68, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination with other AAV8 sequences or in combination with elements from other AAV or non-AAV viral sequences or in combination with elements from other AAV and for use as antisense delivery vectors, gene therapy vectors or vaccine vectors. A claimed molecule comprises a cap protein of a functional AAV rep gene from a serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5 and

Sequence 736

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RESULT 5
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Matches 599
13-NOV-2001;
17-DEC-2001;
01-MAY-2002;
                                                                                                                                                                                                                                                                           adeno-associated virus; AAV; cytostatic; antipsoriatic; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antithyroid; dermatological; antiinflammatory; gene therapy; vaccine; hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
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                                                                                                                                                                                                                                                           autoimmune
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Pred. No. 1.4e-253;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antithyeoid, dermatcological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other autoimmune diseases like rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohm's disease. This sequence represents an AAV related protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting adeno-associated virus sequences in a sample, useful preventing or treating hyperproliferative or autoimmune disease comprises subjecting a sample having a DNA to amplification via polymerase chain reaction.
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Pred. No. 1.4e-253;
Mismatches 0;
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Length Indels

0

Gaps

197

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317 180 257 120

599

480

420 497 360 437 300 377 240

557

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CC virion. Also described are: a polynucleotide encoding the mutated protein composition. Also described are: a polynucleotide encoding the mutated protein composition to a cell or tissue of a vertebrate combined. The recombinant AAV virion is useful for delivering a delivering a recombinant AAV virion is useful for delivering a composition of a cell or tissue of a vertebrate composition in the protein encoded by the heterologous nucleic acid molecule to a cell or tissue of a vertebrate composition of the protein encoded by the heterologous nucleic acid composition of the protein as composition and avoid the neterologous nucleic acid molecule is expressed at a level that provides a therapeutic effect, composition of the protein as composition in the protein that when present in an AAV virion imparts decreased composition as composition as composition and is operably composition of the protein as composition of the protein and is operably composition of the protein. The protein or the recombinant AAV virion as composition of the protein. The protein or the recombinant AAV virion composition is useful for treating or preventing a wide variety of disorders such as hemophilia, phenylketonuria, Crigler-Najjar disease, Gout and Lesch-composition and phenylketonuria, Crigler-Najjar disease, atherosclerosis, cancer, inflammatory and immune disorders, muscular dystrophies, and composition composition as the amino acid sequence of adeno-associated virus in the monitor of the protein or the composition as the amino acid sequence of adeno-associated virus in the composition and instance of adeno-associated virus in the composition or the composition and instance of adeno-associated virus in the composition of the monitorial sequence of adeno-associated virus in the composition of the monitorial sequence of adeno-associated virus in the composition of the monitorial sequence of adeno-associated virus in the composition of the monitorial sequence of adeno-associated virus in the composition of the monitorial sequence of aden
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30-APR-2004; 2004US-0567310P.
03-JUN-2004; 2004US-0576501P.
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29-APR-2004; 2004US-0566546P.
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                  QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                 IWAKI PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                              IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                                                                           VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                                                                                               VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGP
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bacterial infection; cancer; ulcerative colitie; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antidiabetic; anti-HIV; antipsoriatic; vasotropic; gastrointestinal-gen; hemostatic; anti-HIV; virucide; antibacterial; cytostatic; antiulcer; dermatological.
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                                                                                                                                                                                                                                                                                                            scleroderma;
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30-SEP-2004;
                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; multiple sclerosis; sarcoidosis;
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                                                                                                                                                       Adeno-associated virus.
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Crohn's disease; hemophilia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adeno-associated virus protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                         IWAKI PHTDGHFHPS PLMGGFGLKNPPPQI LI KNTPVPANPPAEFSATKFASFI TQYSTG
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Pred. No. 1.4e-253;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an adeno-associated virus (AAV) clade compris at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuris by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, arcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
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antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
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29-APR-2004;
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ilarity 100.0%;
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The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoB) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV7 or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoB or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is
                                                                                                                                                         Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an AAV serotype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
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                                               IWAKI PHTDGHFHPS PLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                        IWAKIPHTDGHFHPSPLMGGFGLKNPPPOILIKNTFVPANPPABFSATKFASFITQVSTG
                                                                                          VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19;
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antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; a
virucide; antibacterial; cytostatic; antiulcer; dermatological.
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                                                                                                                                                                                                                                                                                                              Sequence
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29-APR-2004;
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Pred. No. 6.9e-252;
3; Mismatches 2;
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                                                                                                                                  30-SEP-2003; 2003US-0508226P 29-APR-2004; 2004US-0566546P
                           New adeno-associated virus (AAV) clade comprising at least three A members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bact
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Best Local Similarity
Matches 596; Conserv
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Pred. No. 6.9e-
0; Mismatches
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QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL

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28-MAR-2001 (first

AAV6 capsid protein ٧p1

AAB59847
ID AAB59
XX AAB59
AC AAB59
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XX AAV6
plood gene therapy; AAV viral vector; cystic fibrosis; osclerosis; sickle cell anaemia; thalassaemia; clotting disorder; diabetes; capsid protein VP1. clotting disorder; AIDS;

Claim

SEQ

ij

NO 158;

569pp;

English

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Query Match
Best Local Simi
Matches 594;
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Pred. No. 8.3e-252;
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TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA

Query Match Best Local S Matches 594

Similarity

99.3%;

Score 3229; DB 7; Pred. No. 8.3e-252; 3; Mismatches 2;

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                                                            The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic, antipsoriatic, antirheumatic, antiarthritic, neuroprotective, antigsoriatic, antithyroid, dermatological, and antiinflammatory. The AAV sequence can be used in gene therapy or as part of a vaccine to treat disorders. The method is useful in detecting and/or identifying AAV sequences and isolating novel sequences that are identified. The sequences may be used e.g. for preventing or treating hyperproliferative conditions such as cancers and psoriasis, and other aucoimmune diseases they rheumatoid arthritis, multiple sclerosis, diabetes, autoimmune thyroiditis, scleroderma or Crohn's disease. This sequence represents an CAAV related protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-2001;
17-DEC-2001;
01-MAY-2002;
05-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via polymerase chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes; autoimmune thyroiditis; scleroderma; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adeno-associated virus; AAV; cytostatic; antipsoriatic; antiarthritic; neuroprotective; antidiabetic; antithyroi dermatological; antilinflammatory; gene therapy; vaccine;
      Sequence
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                                                                                                                                                              19-JUN-2003; : 30-APR-2004; : 03-JUN-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive; gene therapy; immunogenicity; virus inactivation; hemophilia; Pepck deficiency; galactosemia; phenylketconuria; Crigler-Najjar syndrome; Gout; Zellweger syndrome; ischemia; atherosclerosis; thrombosis; embolism; Parkinson's disease; congestive heart failure; cancer; inflammation; immune disorder;
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                                                           Arbetman AE,
                                                                                                                                                                                                                                                                         21-JUN-2004;
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New mutated adeno-associated virus (AAV) capsid protein that when presen in an AAV virion imparts decreased immunoreactivity to the virion as compared to the corresponding wild-type virion, useful for treating e.g. present

SEQ ID NO 19; 136pp; English

The invention describes a mutated adeno-associated virus (AAV) capsid CC protein that when present in an AAV virion imparts decreased CC immunoreactivity to the virion as compared to the corresponding wild-type CC virion. Also described are: a polymucleotide encoding the mutated protein CC above; a recombinant AAV virion comprising the mutated protein above; and CC delivering a recombinant AAV virion to a cell or tissue of a vertebrate Subject. The recombinant AAV virion is useful for delivering a CC heterologous nucleic acid molecule to a cell or tissue of a vertebrate Subject, where the protein encoded by the heterologous nucleic acid cC where the recombinant AAV virion may comprise a non-primate, mammalian CC AAV capsid protein that when present in an AAV virion imparts decreased immunoreactivity to the virion as compared to immunoreactivity of primate CC AAV-2, and the heterologous nucleic acid molecule encodes a therapeutic protein and is operably CC linked to control elements capable of directing the in vivo transcription and translation of the protein. The protein or the recombinant AAV virion cand translation of the protein. The protein or the recombinant AAV virion imparts decreased companily, glycogen storage deficiency type 1A, pepck deficiency, CC should be applied a phenylketonuria, Crigler-Najjar disease, Gout and Lesch-CC uncleic acid molecule exparkinson's disease, congestive heart failure, CC cancer, inflammatory and immune disorders, muscular dystrophies, and CC (AAV6) capsid protein VP1.

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DB 9; 3.3e-252;

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                               VMITDEEEIKATNPVATERFGTVAVNLQSSSTDPATGDVHVMGALPGMVWQDRDVYLQGP
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Copyright (c) 1993 - 2005 Compugen
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2005, 17:29:19 ; Search time 21.1525 Seconds (without alignments)
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Coat protein - adeno-associated virus type 2

C;Species: adeno-associated virus type 2

C;Pate: 05-Apr-1933 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004

C;Pate: 05-Apr-1933 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004

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A; Accession: $52210
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R;Zadori, Z.; Erdei, J.; Nagy, J.; Kisari, submitted to the EMBL Data Library, Septem
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;Species: muscovy duck parvovirus
;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
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                                                                                                                                                                                                                                 E--SAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALP
                                                                                                                                                                                                                                                                                                                                  SQSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQ
                                                                                                                                                                                                                                                                                                                                                                      YALPQYGYCTMHTNQSGARFNDRSAFYCLEYFPSQMLRTGNNFEFSFEFEEVPFHSMFAH
                                                                                                                                                                                                                                                                                                                                                                                    FMIPQYGYLTLN---NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAH
                                                                                                                                                                                                                                                                                                                                                                                                                       ALKFKIFNVQVKEVTTQDQTKTIANNLTSTIQIFTDNEHQLPXVLGSATEGTMPPFPSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                       RLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEPVNTAPAKKSS----GKLTDHDPIVKKPKLSE----ENSPSPSNSGGEASAAATEGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRPVEQSPQEPDSSSGIGK-TGQQPAKKRLNFGQTGDSESVPDPQPLG---
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                                                                                                 NOKWNSY I TOYSTGOCTVEMVWELRKENSKRWNPEI OFTSNFGNRTSTMFAPNETGGYVE
                                                                                                                                                                  GMVWQDRDVYLQGFIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFS
                                                                                                                                                                                                        DPYRSGSTLAGISDIMVTDEQEIAPTNGVGWRPYGLTVTNEQNTTTAPTNAELEVLGALP
                                                                                                                                                                                                                                                                                       RVSKTK--TDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGK 408
                                             DRLIGTRYLTQNL
                                                                  PRPIGTRYLTRPL 599
                                                                                                                                                    GMVMQNRDIYLQGPIWAKIPKTDGKPHPSPNLGGFGLHNPPPQVFIKNTPVPADPPLEYV
                                                                                                                                                                                                                                                              RVRAYSGGTDNYANWSIWSKGNKVFLKDREYLLQPGPVATTHTEDQASSVPAQNIIGIAK
                                                                                                                                                                                                                                                                                                                 SQDLDRLMNPLLDQYLWNFSEV-NGGRNAQ-----FKKAVKGAFGAMGRNWLPGPKLLDQ
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                                             732
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Pred. No. 1.6e-108;
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  coat protein VPI - parvovirus B19 (stra
C;Species: parvovirus B19
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision
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coat protein VP1 - bovine parvovirus
N;Contains: coat protein VP2
C;Species: bovine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_chang
C;Accession: A26104
R;Chen, K.C.; Shull, B.C.; Moses, E.A.; Lederman, M.; Stout, E
J. Virol. 60, 1085-1097, 1986
A;Title: Complete nucleotide sequence and genome organization A;Reference number: A26104; MUID:87061184; PMID:3783814
A;Accession: A26104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-673 < CHS>
A; Residues: 1-673 < CHS>
A; Cross-references: UNIPROT: P07297; UNIPARC: UPI0000127D77;
C; Superfamily: parvovirus coat protein
C; Keywords: coat protein
C; Keywords: coat protein
F; 138-673/Product: coat protein VP2 #status predicted < VP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 LFNIQVKEVTTNDGVTTIANN-LTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIP ::|:|:|:::|| ::: || ::: || ::: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 AAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEP--PATP
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----AARHTFTREARTKLITGSNGADGDYKEWWMLPNQMWDSAPISRYNPIWVKVP
                                                                                                                                                                                                                                                                                                                                                NGAD----VSGVRAVRVGYSTDPIYGGQQPESDLLRLRYSASAAEGQQNPILEN-----
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                                                   EIEWELQKENSKRWNPEVQYTSNYAKSANVD-FTVDNNGLY
                                                                                                                                                                     HTDGHFHPSPLMGGFGLKUPPPQILIK--NTPVPANPPAEFSATKFASFITQYSTGQVSV 544
                                                                                                                                                                                                                                                                                          EEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GIARGTHNATLQTQSAGALVTMVT
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#text\_change 09-Jul-2004

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A;Title: Nucleotide sequence and genome organization of A;Reference number: A24299; MUID:86200451; PMID:3701931 A;Accession: A24299
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R;Shade, R.O.; Blundell, M.C.; Cotmore, S.F.; Tattersall, J. Virol. 58, 921-936, 1986
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                                                                                                                                                                                                                     coat protein VP1 - porcine parvovirus
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
C;Accession: B33302
R;Ranz, A. I; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.
R;Ranz, Virol, 70, 2541-2553, 1989
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                                                      A;Title: Porcine parvovirus: DNA sequence and genome organization. A;Reference number: A3302; MUID:90010964; PMID:2794971 A;Accession: B3302 A;Molecule type: DNA A;Residues: 1-723 <RAN A;Residues: 1-723 <RA
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Best Local Simi
Matches 148;
Cross-references: UNIPROT:P18546; Genetics:
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ilarity 27.3%;
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Pred. No. 6.2e
84; Mismatches
                                     UNIPARC: UPI0000174964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495; DB 1;
No. 6.2e-26;
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                                     EMBL: D00623
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A; Molecule type: I A; Residues: 1-729

DNA

30-Sep-1993 #text\_change

09-Jul-2004

porcine

parvovirus

<SAK

A;Cross-references: UNIPROT:P33484; UNIPARC:UPI0000127C6E

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coat protein VPI - porcine parvovirus (strain 90HS)
N;Contains: coat protein VP2
C;Species: porcine parvovirus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text
C;Accession: A60006
R;Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
A;Ritle: Nucleotide sequence of capsid protein gene of paragraphy.
A;Reference number: A60006; MUID:89319168; PMID:2750278
A;Accession: A60006
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C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;145-723/Product: coat protein VP2 #s
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A60006
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                                                                                                                                                                                                                                                                                                                                                        DDFNADSPQQPRIITYSNFWWKGTLTFTAKMRSSNMWNPIQQHTT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMHFMNTLNTYGP
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Pred. No. 8.0
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coat protein VP1 - porcine parvovirus (strain NADL-2) N;Contains: coat protein VP2 C;Species: porcine parvovirus C;Date: 31-Dec.1990 #sequence_revision 31-Dec.1990 #text_change C;Accession: B33743; D48472 R;Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W. Virology 173, 368-377, 1989 A;Ritle: Nucleotide sequence analysis of the capsid genes and th A;Reference number: A33743; MUID:90085785; PMID:2596019 A;A;Accession: B33743
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A; Molecule type: DNA
A; Residues: 1-729 < VAS>
A; Cross-references: UNI
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 UNIPROT: P18546; UNIPARC: UPI0000127C70; GB: M32787; NID: g332983;
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22.7%; Pred. No. 1.6e-09;
ative 95; Mismatches 277;
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RESULT VCPVV2

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R;Bergeron, J.; Menezes, J.; Tijssen, P.

Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription and translati
A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Reference number: DNA
A;Rocession: D48472
A;Molecule type: DNA
A;Rosidues: 11-729 + BBER
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:13879;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:13879)
C;Genetics:
A;Introns: 10/1
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein; glycoprotein
C;Keywords: coat protein; glycoprotein
F;151-729/Product: coat protein VP2 #status predicted <VP2>
F;32,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asm
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                                    LYTEPRPIG
                                                          DENADSPOOPRIITYSNEWWKGTLTETAKMRSSNMMNPIQOHTT--
                                                                                                          EFSA-TKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNG
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                                                                                                                                                                                  GMVWQDRDVYLQGPIWAKIPHTD--GHFHPSPLMGGPGLK-NPPPQILIKNTPVPANPPA
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 NYI-PTNIG
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22.7%;
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Pred. No. 1.6e-09;
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C;Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change (C;Date: 14-Nov-1983 #species (man)
R;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nucleotide sequence of H-1 and mappin A;Beference number: A03695; MUID:83112183; PMID:6823009
A;Accession: A03699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-722 <RHO>
A;Crose-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D;
C;Superfamily: parvovirus coat protein
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RESULT 9
844276
coat protein VP1 - parvovirus LuIII
C;Species: parvovirus LuIII
C;Date: 17-Feb-1994 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSFYCLE-YFPSQMLRTGNNFTF-SYTFEEVPFHSSYA----HSQSLDRLMN-PLIDQY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPYVLGSAHQGCL-----PPFPAD---VFMIPQYGYLTLNNGSQ-----AVG----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWQRLINNNWGFRPKRLNFKLFNIQVKEVTT-----NDGVTTIANNLTSTVQVFSDSEYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTW--LGDRVITTSTRTWAL
                                                                                                                                                                   NST
                                                                                                                                                                                                                                                                            PHPDP
                                                                                                                                                                                                                                                                                                              SSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNP
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                                                                                                                                                                                                     -NLTDQFDPNSTTVSRIVT-YSTFYWKGILKFKAKLRPNLTWNPVYQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 244; DB 1;
Pred. No. 8.4e-09;
   17-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                            IYPNGQIWDKELDLEHKPRLHVTAPFV---CKNNP
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A;Reference number: A44276; MUID:93297126; PMID:8517025 A;Accession: B44276
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R;Diffoot, N.; Chen, K.C.; Bates, R.C.; Lederma, Virology 192, 339-345, 1993
A;Title: The complete nucleotide sequence of par
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT: P36310; UNIPARC: UPI0000127D7E;
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A; Residues: 1-587 < DIF>
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Matches 137
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nes 137; Conserv
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                                                                                                  DVHAMGALPGMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKN
                                                                                                                                                                                                                                                                                                                                               RINLLRIGDEVATGTYYFDTEPIRLTHTWQTNRHLGQPPQITELPSSDTANATLTARGYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---RVITTSTRTWAL-
APNLTDQYDPNSSNLSRIVTYGTFFWXGKLTLKAK---MRPNA-TWNPVFQISA
                                                                                                                                                                                                                                                                          YYLNRTON------OSGSAONKD-LLFSRGSPAGMSVQPKNWLPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWWGFRPKRLNFKLFNIQVKEVT-TNDGVTTIA---NNLTSTVQVFSDSEYQLPYVLGSA 221
                                TP--VPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTS
                                                                                                                                                                    VMIFGKESAGASNTALDNVMITDEEEIKATNPVATER---FGTVAVNFQS--SSTDPATG
                                                                                                                                                                                                      LRYTYDKQHGQSWASQNNKDRYTW-DAVNYD-SGR----
                                                                                                                                                                                                                                          ---PCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG
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                                                                     -----PAPIYPQGQIWDKELDLEHKPRLHTQAPFV---CKNNAPGQLLVRL
                                                                                                                                    -WTNNCFIQSVPFTSEPN---ANQILTNRDNLAGKTDIHFTNAFNSYGPLTA
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23.1%;
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Pred. No. 3e-08
74; Mismatches
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R;Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward, D.C. Nucleic Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, A;Reference number: A03696; MUID:83143341; PMID:6298737

an

autonomous

parvovirus

A; Molecule type: DNA A; Residues: 1-716 < AST>

A; Accession: A03700

A; Cross-references: UNIPROT: P03137; UNIPARC: UPI0000127D6D;

EMBL: V01115

coat protein VP1 - minute virus of mice
C;Species: minute virus of mice, murine parvovirus
C;Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983

#text\_change 09-Jul-2004

Accession: A03700

VCPV2M

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A;Title: Cloning and sequence of DNA encoding structural proteins of the autonomous pareterence number: A03697; MUID:85265017; PMID:2991581
A;Accession: A03701
A;Molecule type: DNA
A;Cresidues: 1-727 <CAR>
A;Cresidues: 1-727 <CAR>
A;Cresidues: 1-727 <CAR>
A;Cresidues: CINIPROT:P04864; UNIPARC:UPI0000127D55; EMBL:M10824; NID:g333474; C;Genetics:
                                                                                                      coat protein VP1 - feline panleukopenia virus
N;Contains: coat protein VP2
C;Species: feline panleukopenia virus, FPLV
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_
C;Accession: A03701
C;Accession: A03701
C;Accession: J; Rushlow, K.; Maxwell, I.; Maxwell, F.; Win
J; Virol. 55, 574-587, 1985
A;Title: Cloning and sequence of DNA encoding structural
A;Reference number: A03697; MUID:85265017; PMID:2991581
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VCPV1F
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;Keywords: coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                   -CKNNAPGOMLVRLGPNLTDOYDPNGATLSRIVTYGTFFWKGKLTMRAKLRA----NTTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - PEADTDAGT-----LTAQGSRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFEASRAG
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Pred. No. 6.9e-07;
                                                                                                                                                                                                                                                                                                                                                  -DNGNSYMSVTKWLPTATGNMQSVPLITRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PSPVYPQGQIWDKELDLEHKPRLHITAPFV--
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                                                                                                                                                                 I.; Maxwell, F.; Winston,
                                                                                                                                                                                               FPLV
30-Jun-1987 #text_change
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R;Sahli, R.; McMaster, G.K.; Hirt, B.

Nucleic Acids Res. 13, 3617-3633, 1985

A;Title: DNA sequence comparison between two tissue-specific variants of the autonom A;Title: DNA sequence comparison between two tissue-specific variants of the autonom A;Reference number: A23008; MUID:85242059; PMID:3855242

A;Accession: B23008

A;Molecule type: DNA

A;Residues: 1-718 <SAH>

A;Residues: 1-718 <SAH>

A;Residues: 1-718 <SAH>

A;Residues: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; NID:g60918;
R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.

J. Virol. 57, 656-669, 1986
                                                                                                                                                                                                               coat protein VP1 - minute virus of mice (strain MVMi)
C;Species: minute virus of mice, murine parvovirus
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: B23008; B29510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGPTTMASGGGAPMADNNEGADGVGNASGNWH------CDSTWLGDRVITTSTRTWALP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVMIFGKESAGASNTALD-NVMITDEEBIKATNPVATERFGTVAVNFQSSSTDPATGDVH
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20.2%; Pred. No. 7e-07;
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autonomous

PIDN

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coat protein VP1 - mink enteritis virus (strain )
N;Contains: coat protein VP2
C;Species: mink enteritis virus, MEV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-199
C;Accession: B38350
R;Kariatsumari, T; Horiuchi, M.; Hama, E.; Yagud, Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence and A;Reference number: A38350; MUID:91202123; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: DNA sequence of the lymphotropic \
A;Reference number: A29510; MUID:86115415;
A;Accession: B29510
A;Molecule type: DNA
A;Residues: 1-143,'A',145-718 <AST>
A;Cross-references: UNIPARC:UPI0000127D6C;
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
                                                                                                                                                                 RESULT
VCPVME
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Best Local Simi
Matches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVEQSPQEPDSSSGIGKTG-------QQPAKKRLNFG---QTGDSESVPDPQPLG
                                                                                                                                                                                                                                                                                                                                                                                      GPLTAFSH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PEADTDAGT-----LTAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNSQFFTIENTQQITLLRTGDEFATGTYYFDTNPV--KLTHTWQTNRQLGQPPLLSTF--
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                                                                                                                                                                                                                                                                                                              MLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRA----NTTWNPVYQ----
                                                                                                                                                                                                                                                                                                                                                ILIKNTP---VPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSN
                                                                                                                                                                                                                                                                                                                                                                                                                      DPATGDVHAMGALPGMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDGFIQSAPLVVPPPLNGILTNA------NPIGTKN----DIHFSNVFNSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- FPMSGVMI FGKESAGASNTALDNVMI TDEEEI KATNPVATERFGTVAVNFQS--
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Pred. No. 8.7e
B9; Mismatches
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1. No. 8.7e-07;
1. no. e.7e-07;
2. no. e.7e-07;
2. no. e.7e-07;
                                                                                          30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                (strain
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     nce analysis of PMID:2016597
                                                        Yaguchi, K.; Ishigurio, N.;
                                                                                                                                                Abashiri)
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                            of the
                                                              Shinag
                                                                                             coat protein VP1 - feline panleukopenia virus NyContains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 31-Dec-1991 #sequence_revision 31-Dec-C;Accession: B36608
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A;Molecule type: DNA
A;Residues: 1-722 <KAR>
A;Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
       R;Martyn, J.C.; Davidson, B.E.;
J. Gen. Virol. 71, 2747-2753, 19
A;Title: Nucleotide sequence of
A;Reference number: A36608; MUII
A;Accession: B36608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSAQNKDLLFSRGSPAGMS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCL-----PPFPA------DVFMIPQYGYLTLNNGSQAVGRS-----SFYCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGPTTMASGGGAPMADNNEGADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALP
                                                                                                                                                                                                                                                               SIN------VDNQFNYL-PNNIG
                                                                                                                                                                                                                                                                                                 TSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                                                                                                     POILIKNTPVPAN---PPAEFSATKFASFITOYSTGOVSVEIEWELQKENSKRWNPEVOY
                                                                                                                                                                                                                                                                                                                                                                                                            ALNNVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                            AMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVMIFGKESAGASNTALD-, VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVH
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                                                                                                                                                                                                                                                                                                                                       GQLFVKVAPNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQM
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                              e of feline panleukopenia virus: MUID:91073139; PMID:2174965
                                                                   1990
                                                                             Studdert, M.J.
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Pred. No. 9.5e-07;
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R:Parrish, C.R.; Aquadro, C.F.; Carmichael, L.E. Virology 166, 293-307, 1988
A;Title: Canine host range and a specific epitope map along A;Reference number: A31163; MUID:89020796; PMID:3176341
A;Accession: A31163
                                                                                              coat protein VP1 - canine parvovirus (e %Contains: coat protein VP2 C;Species: canine parvovirus, CPV C;Date: 31-Mar-1990 #sequence_revision C;Accession: A31163
                                                                                                                                                                                 RESULT
VCPVCD
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A;Residues: 1-727 <max>
A;Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
A;Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted <VP2>
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPESENYKRVVVNNMDKTAVKGNMALDDIHVQIVTPWSLVDANAWGVWFNPGDWQLIVNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGPTTMASGGGAPMADNNEGADGVGNASGNWH-----CDSTWLGDRVITTSTRTWALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
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                                                                                                                                                                                                                                                    SIN----
                                                                                                                                                                                                                                                                                 TSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                                                 GQLFVKVAPNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTWNPIQQM
                                                                                                                                                                                                                                                                                                                                               PQILIKUTPVPAN---PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQY
                                                                                                                                                                                                                                                                                                                                                                                   ALMNVP-----PVYPNGQIWDKEFDTD----
                                                                                                                                                                                                                                                                                                                                                                                                                  AMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGRGGAQTDENQAA----DGDPRYAFGRQHGQKTTTTGETPERFTYIAHQDT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETLGEYPWKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNVYHGTDPDDVQFYTI
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A;Residues: 1-737 <PAR>
A;Cross-references: UNIPROT:P17455; UNIPARC:UPI0000127D7A; EMBL:M23255; NID:g333467; PID
C;Genetics:
C;Genetics:
A;Introns: 26/3
A;Introns: 26/3
C;Superfamily: parvovirus coat protein
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPTKRSKPPPHIFINLAK-----KKKAGAGQVKRDNLAPMSDGAVQPDGGQPAVRNERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCL-----PPFPA------DVFMIPQYGYLTLNNGSQAVGRS-----SFYCL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWGFRPKRLNFKLFNIQVKEVI---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQ 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPESENYRRVVVNNMDKTAVNGNMALDDIHAQIVTPWSLVDANAWGVWFNPGDWQLIVNT
                                                                  CONNCPGOLFVKVAPNLTNEYDPDASANMSR----IVTYSDFWWKGKLVFKAKLRASHTW
                                                                                                                                                                                                                                                                                                                                                                                                                                          E-YFPSQMLRTGNNF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQ 315
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                                 NPEVOYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                  --- NPPPQILIKNTPVPAN---- PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRW
                                                                                                                                     TYGPLTALNNVP-----PVYPNGQIWDKEFDTD------
                                                                                                                                                                                                    ERFTYIAHQDTGRYPEGDWIQNINFNLPVTNDNVLLPTDPIG----GKTGINY--TNIFN
                                                                                                                                                                                                                                                                     VGYSAPYYSFEASTQGPFKTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETP
                                                                                                                                                                                                                                                                                                                                         EGATNFGDI ----GV---
                                                                                                                                                                                                                                                                                                                                                                       SGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNF-----TW
                                                                                                                                                                                                                                                                                                                                                                                                          ENSVPVHLLRTGDEFATGTFFFDCKP--CRLTHTWQTNRALGLPP-----FLNSLPQS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETLGFYPMKPTIPTPWRYYFQWDRTLIPSH-----TGTSGTPTNIYHGTDPDDVQFYTI
NPIQQMSIN--
                                                                                                                                                                    ATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
                                                                                                                                                                                                                                                                                                        TGASKYNLNGRESIINP-----GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD--
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WEDLINE-99214308; PubMed=10196295;

Wish W. Chirmule N., Berta S.C., McCullough B., Ga Yiao W., Chirmule N., Berta S.C., McCullough B., Ga Yiao W., Chirmule N., Berta S.C., McCullough B., Ga "Gene therapy vectors based on adeno-associated vir J. Virol. 73:3994-4003(1999).

J. Virol. 73:3994-4003(1999).

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J. Virol. 73:3994-4003(1999).

GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule activity; IEA GO; GO:0005198; F:structural molecule act
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Result No.

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Match Query

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PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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NSNFTWTGASKYNLNGRES I INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDN
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SMR; O56137; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 736 AA; 81411 MW; 311217A089C565F5
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MEDLINE=98080418; PubMed=9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
Ruflectious clones and vectors derived from
(AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).
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Best Local Similarity
Matches 592; Conserv
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J. Virol. 78:6381-6388(2004).

BMBL; AY530609; AAS99294.1; -; Genomic_I
SMR; Q6JC10; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule ac
InterPro; IPR001403; Parvo coat.

Pfam; PF00740; Parvo coat; 1.
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Wilson
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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EMBL; AY530606; AAS99291.1; -; Genomic_DNA
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GG; GO:0019028; C:viral capsid; IEA.
GG; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 737 AA; 81332 MW; 94CED0F3AFD6E492
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   NNSNFTWTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALD
                                                                      PLIVQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMS
                                                                                                                                                                                                                   FNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQY
                                                                                                                                                                                                                                                                                         YKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKL
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Pred. No. 5.7e-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94CED0F3AFD6E492 CRC64;
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Best Local Similarity 85.7%;
Matches 514; Conservative 3.
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01-JUN-1998 (TrEMBLrel. 06,
01-MAR-2004 (TrEMBLrel. 26,
Capsid protein VP1.
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MEDLINE=98080418; Pubmed=9420229;
MEDLINE=98080418; Pubmed=9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
"Infectious clones and vectors derived from
"Infectious clones and vectors derived from
"ANU serotypes other than ANV type 2.";
J. Virol. 72:309-319(1998).
EMBL; AF028705; AAB95452.1; -; Genomic_DNA.
SMR; O56139; 217.736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0019028; C:viral capsid; IEA. GO; GO:0005198; F:structural molecule InterPro; IPR001403; Parvo_coat. Pfam; PF00740; Parvo_coat; 1. SEQUENCE 736 AA; 81906 MW; DD52331
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Viruses; ssDNA viruses;
NCBI_TaxID=68742;
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GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                     PIWAKI PHTDGHFHPSPLMGGFGLKNPPPQILI KNTPVPANPPAEFSATKFASFITQYST
GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSASVDFTVDNNGLYTEPRPIGTRYLTRPL
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Parvoviridae; Created)
Last sequence update)
Last annotation update) Parvovirinae; 736 ጅ Dependovirus

from adeno-associated virus

; Score 2832; DB 2; ; Pred. No. 4.8e-187; 34; Mismatches 50; DD52331AD5F0D70F CRC64; 50; Length Indels 2 Gaps

activity;

ΙEΑ

VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY TAPGKKRPVDQSPQEPDSSSGVGKSGKQPARKRLNFGQTGDSESVPDPQPLGEPPAAPTS TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD LIDQYLYYLNRTQ-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDN YLTLANGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLFYVLGSAHQGCLPFFFADVFMIFQYG LIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSNSLQARNWLPGPCYRQQRLSKTANDN KQISSQS-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKKLSFKLF KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF LGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLY NIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYG YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNP 197 60 496 120 419 359 300 180 257 556 436 376 240

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RESULT 8
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DE Capsid protein v
GN Name=cap;
OS Adeno-associated
OC Viruses; ssDNA v
OX NCBI_TAXID=27263
RN [1]
RP NUCLEOTIDE SEQUE
RA Chen C.L., Jense
RA Chen C.L., Jense
RA Sferra T.J., She
RT "Characterizatio
RL Submitted (JUL-2
DR SMR; O670Q8; 217
DR GO; GO:0019028;
DR GO; GO:005198;
DR GO; GO:005198;
DR Ffam; PF00740; F
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SMR; Q670Q8; 217-735.

SMR; Q670Q8; 217-735.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; pF00740; Parvo coat; 1.

SEQUENCE 735 AA; 81887 MW; 258BFB955F1C9925 CRC64;
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Viruses; ssDNA viruses;
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                                                                                                                                            YLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP
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 VMITDEEEIRTTNPVATEQYGNVSNNLQNSNTAPSTGTVNHQGALPGMVWQDRDVYLQGP
                                                                    NSNFPWTAATKYHLNGRDSLVNPGPPMASHKODEEKFFPWHGTLIFGKEGTNANNAELEN
                                                                                         NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
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Query Match
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Matches 506; Conserv
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J. Virol. 78:6381-6388(2004).
EMBL; AY530591; AAS99276.1; -; Genomic_DNA.
SMR; Q6JC28; 217-735.
G0; G0:0019028; C:viral capsid; IEA.
GO; G0:0005198; F:structural molecule activity; IE
InterPro; IPR001403; Parvo_Coat.
Pfam; PF00740; Parvo Coat: 1.
SEQUENCE 735 AA; 81897 MW; 197066F8911FAE98 CR
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28 9VIRU
06JC28 9VIRU F
06JC28;
06JC28;
075-JUL-2004
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                                                                                                                                                                 LIDQYLYYLNKTQTNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGPCYRQQRLSKQANDNN
                                                                                              LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKWWLPGPCYRQQRVSKTKTDNN
                                                                                                                                      YLTLANGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLANP
                                                                                                                           YLTLINIGSQAVGRSPFYCLEYFPSQMLRTGNNFQFSYTFEDVPFHSSYAHSQSLDRLMNP
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Pred. No. 2.5
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RESULT 10
Q6JC34 9VIRU
Q6JC34 9VIRU PRELIMINARY;
AC Q6JC34;
AC Q6JC34;
DT 05-UUL-2004 (TrEMBLrel. 27,
DT 05-UUL-2004 (TrEMBLrel. 27,
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DR Name-cap;
OS Adeno-associated virus.
OC Viruses; ssDNA viruses; Par
OX NCBI_TAXID=272636;
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CN NCBI_TAXID=272636;
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CN NCBI_TAXID=272636;
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CN NCBI_TAXID=272636;
RN [1]
CN NCBI_TAXID=272636;
RN UCLEOTIDE SEQUENCE.
RA WOCLEOTIDE SEQUENCE
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RA GAOGG, COUNT
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A Wilson J.M.;

T "Clades of Adeno-associated viruses are widely disse
IT tissues.";

IL J. Virol. 78:6381-6388(2004).

REMBL; AY530585; AAS99270.1; -; Genomic_DNA.

DR SMR; Q6JC34; 217-735.

DR GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IE/

DR InterPro; IPR001403; Parvo_coat.

DR Pfam; PF00740; Parvo_coat; 1.

SO SEQUENCE 735 AA; B1962 MW; 85DC69C55232D983 CF
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PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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                  VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGP
                                                                                 NIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYG
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84.5%; Pred. No. 3e-1
Live 41; Mismatches
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.R., Lu Y., Calcedo
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AC Q6JBZ1 05-JUL-2
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Matches 506;
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05-JUL-2004
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EMBL; AY530628; AAS9313.1; -; Genomic_DNA.

SMR; Q6JBZ1; 217-735.

G0; G0:0019028; C:viral capsid; IEA.

G0; G0:0005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat.

SEQUENCE 735 AA; 81868 MW; 1654ED66287F5474 CRC64;
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Name=cap;
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                     VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                                                           NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN
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                                                                                      NSNFPWTAATKYHLNGROSLVNPGPAMASHKODEEKFFPMHGTL1FGKQGTNANDADLDN
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ilarity 84.5%;
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Pred. No. 4.1e-
40; Mismatches
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EMBL; AY530622; AA599307.1; -; Genomic_DNA.

SMR; OGJBE7; 217-735.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity;

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 735 AA; 81947 MW; EBA318E904E0BF0A
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06JBZ7;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
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NCBI_TaxID=272636;
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84.3%; Pred. No. 4.1e-186;
tive 41; Mismatches 52; Indels
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Best Local Similarity
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Adeno-associated virus 3.
Viruses; ssDNA viruses; I
NCBI TaxID=46350;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat; 1.
SEQUENCE 736 AA; 81660 MW; AFF1EF47B5C67A10
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Q65311;
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Muramatsu S., Mizukami H., Young N.S., Brown K.E.;
"Nucleotide sequencing and generation of an infectious casociated virus 3.";
virology 221:208-217(1996).
EMBL; U48704; AAC55049.1; -; Genomic_DNA.
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Wilson J.
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J. Virol. 78:6381-6388(2004).

BMBL; AY530602; AAS99287-1; -; Genomic_DNA.

SMR; Q6JC17; 217-735.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0015198; F:structural molecule activity;
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat. 1.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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"Clades of Adeno-associated viruses are widely tissues.";
J. Virol. 78:6381-6388(2004).
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EMBL; AY530581; AAS99266.1; -;
SMR; Q6JC38; 217-735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adeno-associated virus. Viruses; ssDNA viruses;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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SEQUENCE 735 AA; 81913 MW; 5
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                              VMITDEESIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
                                                                    LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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VMITDESEIRTTNPVATEQYGYVSNNLQDSNTGPTTGTVNHQGALPGMVWQDRDVYLQGP
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Search completed: November 23, 2005, 17:41:18 Job time : 117.377 secs	677 OVSVETEWELD	541 QVSVEIEWELQ	617 IWAKIPHTDGHE	481 IWAKIPHTDGHE
c 23, 2005, 17:41:18	677 OVSVETEWELOXENSKEWIDETOYTSNYNKSVNVDETVDTNGVYSEPRPIGTRYLTENI. 735	541 QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599	617 IWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTG 676	481 IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPABFSATKFASFITQYSTG 540

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Result
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3251
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Listing first 45 summaries
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    GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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APPLICANT: Xiao, Weidong

APPLICANT: Xiao, Weidong

TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,

TITLE OF INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN.031USA

CURRENT APPLICATION NUMBER: US/09/807,802A

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 736

TYDE: PRT

ORGANISM: AAV-1
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5. 6759237
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NSNFTWTGASKYNLNGRESIINPGTAMASHKDDBDKFFPMSGVMIFGKESAGASNTALDN
                                                                                                       LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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                                                                              LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
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SEQ ID NO 13
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ORGANISM: AAV-1
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VMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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QVSVETEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                            QVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                                            IWAKI PHTDGHFHPS PLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
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APPLICANT: Wilson, James M.
APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02 Length Sequences,

1 TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA 60 Indels 0, Gaps

TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPAA 197 VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY 120 KQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLF 180 VGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLY 257

NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG NIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYG 377 240

YLTLANGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNP 300 LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN 360

NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN 420 NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDN LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN 497

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wilson, James M.

APPLICANT: Xiao, Weidong

ITITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequentiate Of INVENTION: Vectors and Host Cells Containing Same

FILE REFERENCE: GNVPN 031USA

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,802A

CURRENT FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: US 60/107,114

PRIOR APPLICATION NUMBER: PCT/US99/25694

PRIOR FILING DATE: 1999-11-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1

SEQ ID NO 17

LENCTH: S34

TYPE: PRT

ORGANISM: AAV-1

US-09-807-802A-17
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US-09-807-802A-17
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Best Local Similarity
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                                                                                                                                                              WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD 425
                                                                                                                                                                                                                                        LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKWKLPGPCYRQQRVSKTKTDNNNSNFT 365
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                                                                                                    BEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAKI
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                            PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                              PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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RESULT 6 US-10-293-478-1

Sequence 1, Application Patent No. 6733757 GENERAL INFORMATION:

US/10293478

APPLICANT: PATEL,

SALIL

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APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPILE OF INVENTION: ADENO-ASSOCIATED VIRUS CAPILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/09/321,589
CURRENT FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
TYPE: PRT
ORGANISM: Adeno-associated virus
US-09-321-589-1
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US-09-321-589-1
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Best Local Similarity
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QVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
            OVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599
                                              IWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                                                 WITDEEEIRTINPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGP
                                                                                                                VMITDEBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.0%; Score 2764.5; DB 2;
82.8%; Pred. No. 3.3e-237;
Live 43; Mismatches 59;
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APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS C
FILE REFERENCE: 39672
CURRENT APPLICATION NUMBER: US/10/293,478
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/321,589
PRIOR TILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
TYPE: PRT
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Best Local S
Matches 496
                                                                                                                            Sequence 13, Application Patent No. 6962815 GENERAL INFORMATION:
          APPLICANT: J. BARTLETT APPLICANT: J. BARTLETT TITLE OF INVENTION: AAV VECTORS AND METHODS FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Adeno-associated virus
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                                                                                                                                                                US/10038972F
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SEQ ID NO 13
LENGTH: 735
TYPE: PRT
ORGANISM: adeno-associated
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LIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNN
                                                                             IWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG
                                                                                                                            VMITDBBEIKATNPVATERFGTVAVNFQSSSTDFATGDVHAMGALFGMVWQDRDVYLQGF
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                                                                                                                                                                  NSEYSWTGATKYHLNGRDSLVNPGPAMASHKDDEEKFFPQSGVLIFGKQGSEKTNVDIEK
                                                                                                                                                                                                                   LIDQYLYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNN
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                                                     IWAKI PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTG
                                                                                                           VMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGP
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82.8%;
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Pred. No. 3.36
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3.3e-237;
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US-10-038-972A-14
; Sequence 14, Application US/10038972A
; Patent No. 6962815
; GENERAL INFORMATION:
APPLICANT: J. Bartlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/36996US
; CURRENT EPLING DATE: 2002-01-04
; PRIOR REPLICATION NUMBER: US/10/038,972A
; CURRENT FILING DATE: 2002-01-04
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14
; LENGTH: 598
; TYPE: PRT
CORGANIZSM: adeno-associated virus 2 VP2 capsid protien
US-10-038-972A-14

Query Match

.9%; Score 2759.5; DB 2; Length 5:

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Sequence 15, Application US/10038972A
Patent No. 6962815
GENERAL INFORMATION:
APPLICANT: J. BARTLETT
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 533
TYPE: PRT
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                                   MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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 ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 185
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                                                                       76.3%; Score 2481.5; DB 2; ilarity 83.3%; Pred. No. 3.2e-212; Conservative 37; Mismatches 51; 1
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                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP2 US-09-532-594B-16
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US-09-532-594B-16
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CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 598
LENGTH: 598
                                                                                                                                                 Query Match
Best Local S
Matches 355
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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   Conservative
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WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
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                                                                        PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                                                                                                                                                                                                                                             LYYLSRTNTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS
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                                                                                                                                                                           EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
IEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2 MSDDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHL AVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL TAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSG-----A TAPGKKRPVEOSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESVPDPQPLGEPPATPA 59 Score 1830.5; DB 2; Pred. No. 3.7e-154; 4; Mismatches 154; Sequence; Length No. 598; 6468524e 31; Gaps

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GENERAL INFORMATION:

APPLICANT: Chorini, John A.

APPLICANT: Kotin, Robert M.

APPLICANT: Safer, Brian

APPLICANT: Safer, Brian

APPLICANT: Davidson, Beverly

APPLICANT: Davidson, Beverly

TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF

FILE REFERENCE: 14014.0252U2

CURRENT APPLICATION NUMBER: US/09/532,594B

CURRENT FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 734

TYPE: PRT
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US-09-532-594B-4
                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09532594B Patent No. 6468524
                                                                                                                                                                                                                                                                                                                                                                                                ·09-532-594B-4
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence; No. 6468524e OTHER INFORMATION: Synthetic construct NAME/KEY: misc feature NAME/KEY: misc feature OTHER INFORMATION: AAV4 capsid protein VP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525
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                                                    191 MSDDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGHVTTTSTRTWVLPTYNNHL
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                                                                                 AVGPTTMASGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHL 119
                                                                                                                                                                                                TAPGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNF-GQTGDSESVPDDPQPLGEPPATPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPRPIGTRYLTRPL 599
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YKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPRAIGTRYLTHHL
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                                                                                                                                                                   TAPGKKRPLIESPQQPDSSTGIGKKGKQPAKKKLVFEDETGAGDGPPEGSTSG-----A
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                            56.3%; Score 1830.5; DB 2; 57.8%; Pred. No. 5.2e-154; ative 74; Mismatches 154;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-533-427-5
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Davidson, Elizabeth
APPLICANT: Javidson, Eliz
                                                                                                                                                                                                                                                    Query Match 52.3%; Score 1700.5; DB 2; Best Local Similarity 55.0%; Pred. No. 1.4e-142; Matches 332; Conservative 64; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Appli
Patent No. 685531
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
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                                                          GPTIMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09533427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGAL 465
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                          GADTMSAGGGGDLGDNNQGADGVGNASGDWHCDSTWMGDRVVTKSTRTWVLPSYNNHQYR
                                                                                                                                                                                             PGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPA-AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYT
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                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence:/No.synthetic construct
                                                                                                                                           DAEAGPSGSQQLQIPAQPASSL
                                                                                                                                                                                                                                                       Indels
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AND LUNG

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35;

Gaps

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GENERAL INFORMATION:

APPLICANT: Chiorini, John

APPLICANT: Kotin, Robert M.

APPLICANT: Kotin, Robert M.

APPLICANT: Davidson, Elizabeth

APPLICANT: Davidson, Elizabeth

APPLICANT: Zabner, Joseph

TITLE OF INVENTION. AAV5 VECTOR FOR TRANSDUCING BRA

FILE REFERENCE: 14014.0323U2

CURRENT APPLICATION NUMBER: US/09/533,427

CURRENT FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 724

TYPE: PRT

ORGANISM: Artificial Sequence
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US-09-533-427-4
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                                                                                                                                   Query Match
Best Local :
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                                                                                                                       Matches
                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e OTHER INFORMATION: synthetic construct
                                                                                                                                     Local Similarity
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                                                                                     PGKKRPVEQSPQEPDSSSGIGKTGQQPAKKRLNFGQTGDSESVPDPQPLGEPPATPA-AV
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GPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYK 121
                                                          Conservative
                                                                                                                                     52.3%;
55.0%;
                                                                                                                     Score 1700.5; DB 2;
Pred. No. 1.9e-142;
4; Mismatches 173;
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STGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKE 186

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APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VCCTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
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                                                                                                                              OTHER INFORMATION: Description of Artificial OTHER INFORMATION: synthetic construct NAME/KEY: misc_feature OTHER INFORMATION: AAV4 capsid protein VP3 US-09-532-594B-18
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US-09-532-594B-18
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                                                               Matches
                                                                                              Query Match
                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                               52.0%; Score 1690.5; DB 2, Local Similarity 59.4%; Pred. No. 9.6e-142; nes 325; Conservative 65; Mismatches 132;
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GENERAL INFORMATION:
APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
APPLICANT: Zabner, Joseph
FILE REFERENCE: 14014.0323U2
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 532
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-533-427-6
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 318; Conserv
                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: synthetic construct
-09-533-427-6
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                                                                          ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK 185
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GVDGSNANAYFGYSTEWGYFDFNRFHSHWSPRDWQRLINNYWGFRPRSLRVKIFNIQVK
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                                                                                                                                              51.2%; Score 1665; DB 2; 58.9%; Pred. No. 1.7e-139; tive 54; Mismatches 154;
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               GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 599
                                                         PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVS8FITQYST
                                                                                                                   NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEIVPGSVMMERDVYLQG
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GQVTVEMEWELKKENSKRWNPBIQYTNNYNDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL
                                                                         PIWAKIPHTDGHFHPSPLMGGFGLKNPPPOILIKNTPVPANPPABFSATKFASFITQYST
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Search completed: November Job time: 29.2418 secs 23, 2005, 17:42:48

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Adeno-ass	Adz27006	) ADZ27006	735		2506.5	<b>4</b> 5
Adeno-ass	AGZ27037	ADZ27037	734	.4	2511	44
Adeno-ass	Adz27035	Ī		5	2513.5	43
Adeno-ass	Adz26999		735 9	Մ	2514.5	42
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Adeno-ass	Adz27036	ADZ27036		٠	2517	6
Adeno-ass	Adz27004	ADZ27004	735 9	.7	2520.5	39
Adeno-ass	Adz26991	) ADZ26991		. 7	2520.5	38
Adeno-ass	Adz27002	ADZ27002			2522.5	37
Adeno-ass	Adz26998	ADZ26998	735 9	.9	2524.5	36
Adeno-ass	Adz27003	ADZ27003	735	٠,	2524.5	ω 5
Adeno-ass	Adz26992	ADZ26992	735		2527.5	<b>4</b>
Adeno-ass	Adz27067	ADZ27067	736 9		2528	33
Amino aci	Adv67507	ADV67507	736 9		2528	32
Adeno-ass	Ade76572	1 ADE76572	736		2528	31
Adeno ass	Abr62763	1 ABR62763	736		2528	30
AAV3 vp1	Abb80233	ABB80233	736 6		2528	29
	Aab59845	AAB59845	736 4		2528	28
Adeno-ass	Adz27000	ADZ27000	735 9		2529.5	27
Adeno-ass	Adz27076	ADZ27076	735 9		2529.5	26
Vacing-doo	AGZZ/OOL	AU227001	/35	c	2529.5	25

## ALIGNMENTS

RESULT 1 AAY71169 Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy; vaccine; transgene; VP3. 08-SEP-2000 (first entry) AAY71169 standard; protein; 534 AA. WO200028061-A2 Adeno-associated virus 1. Adeno-associated virus serotype 1 capsid protein VP3 AAY71169; 18-MAY-2000.

02-NOV-1999;

05-NOV-1998; 98US-0107114P 99WO-US025694.

(UYPE-) UNIV PENNSYLVANIA.

Wilson JM, Xiao W;

N-PSDB; AAD00772, AAD00779. WPI; 2000-376571/32

Novel adeno-associated virus serotype 1 polynucleotide useful for  ${\sf preparation}$  of medicament for delivery of a transgene to a host.

Claim 7; Page 99-101; 108pp; English.

The patent discloses an adeno-associated virus serotype 1 (AAV-1) DNA which is characterised by two inverted terminal repeats (ITR) and open reading frames for rep and cappid (cap) proteins. The rep reading frame encodes four proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap reading frame encodes three structural proteins, VP1, VP2 and VP3. The AAV-1 sequence or its fragments particularly ITRs, rep and cap coding regions, are useful in production of recombinant viral vectors for gene delivery. These vectors can be used as gene therapy vectors, vaccine vectors or antisense delivery vectors. The AAV-1 does not induce the formation of neutralising antibodies specific to any serotype of AAV hence is useful for transforming host cells, and in the preparation of services. of a

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Best Local Similarity 100
Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                                                   Adeno-associated virus serotype 1; AAV-1; rep protein; capsid protein; cap protein; recombinant viral vector; gene delivery; gene therapy;
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                                                                                                                                                                                                                                                                             Adeno-associated virus 1.
                                                                                                                                                                                                                                                                                                                            vaccine; transgene;
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                                                                                                                                                                                                                                                                                                                              VP2.
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Pred. No. 8e-236;
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RESULT 3
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AAY71167 AAY71167;

standard; protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC which is characterised by two inverted terminal repeats (ITR) and open CC reading frames for rep and capsid (cap) proteins. The rep reading frame for rep and capsid (cap) proteins. The rep reading frame common proteins, Rep 78, Rep 68, Rep 52 and Rep 40, while the cap CC encodes four proteins, Rep 79, Rep 68, Rep 52 and Rep 40, while the cap CC dalvers, are useful in production of recombinant viral vectors for gene CC delivery. These vectors can be used as gene therapy vectors, vectore common of neutralising antibodies specific to any serotype of AAV CC formation of neutralising antibodies specific to any serotype of AAV CC medicament for the delivery of transgene to a host. The present sequence is an AAV-1 cap protein VP2 which is useful in the production of recombinant viral vector for gene delivery
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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DB; AAD00772, AAD00778.
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                                                                                                                                                                                                                                                                  LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                                                                                                                 NGSQAVGRSSFYCLEYFDSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
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EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAKI
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                                                                               PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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                                                              PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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Pred. No. 9.4e-236;
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel adeno-associated virus serotype 1 polynucleotide useful for preparation of medicament for delivery of a transgene to a host.
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N-PSDB; AAD00772, AAD00777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparation
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                     NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                           EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
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 WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD 360
                                                  LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                  NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                      EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                   LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
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Matches 534
                                                                                                                                                                                     The sequences given in ABB80231-34 represent vpl proteins derived from various adeno-associated virus (AAV) serotypes. These sequences were used in the scope of the invention for comparison with the cap protein derived from AAV serotype 9. The AAV capsid comprises three proteins vpl, vp2 and vp3, which are alternative splice variants. The AAV or the nucleic acid molecule is useful for preparing a medicament for delivering a transgene
                                                                                                                                                                                                                                                                                                   New isolated adeno-associated virus (AAV) comprising an AAV9 capsid, useful for preparing a medicament for delivering a transgene to a ce
                                                                                                                                                                                                                                                                                                                                                                     Gao
                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2001;
05-JUN-2002;
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              ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSBRDWQRLINNNWGFRPKRLNFKLFNIQVK 120
                                                MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKOISS
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 ASTGASNONHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                               100.0%; Score 2906; DB 6; llarity 100.0%; Pred. No. 1.3e-235; Conservative 0; Mismatches 0;
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     The present sequence is the protein sequence of the vpl capsid protein adeno associated virus serveype 1 (AAVI). The invention provides the nucleic acid and amino acid sequences of novel AAV8 and fragments of these sequences. Each of these fragments may be used in a variety of vector systems and host cells. Among the desirable fragments are the coproteins, including vpl, vp2, vp3 and hypervariable regions, the sequences including tep78, rep68, rep52 and rep40, and the sequences encoding these proteins. The fragments may be used alone, in combination
                                                                                                                                                                                                                                  Gao
                                                                                                                                             New adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence of AAV8, useful for preparing a medicament for delivery of a transgene to a cell and for treating cystic fibrosis or hemophilia B.
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01-MAY-2002; 2002US-0377133P
05-JUN-2002; 2002US-0386122P
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hyperproliferative; cancer; psoriasis; autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
                                                                                                 antiarthritic; neuroprotective; antidiabetic; antithyroid;
dermatological; antiinflammatory; gene therapy; vaccine;
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                                                                                                                      adeno-associated virus; AAV; cytostatic; antipsoriatic;
                                                                                                                                          Adeno-associated virus (AAV)
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05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for detecting adeno-associated virus (AAV) sequences in a sample, which comprises subjecting a sample containing a DNA to amplification via a polymerase chain reaction (PCR). The AAV sequence have the following activities: cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting adeno-associated virus sequences in a sample, useful for preventing or treating hyperproliferative or autoimmune diseases, comprises subjecting a sample having a DNA to amplification via
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                             LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                                           NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                                       EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                                                                                                                                                                                                                                                                                                                                                                   ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                      WTGASKYNINGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                                                                                                                                             LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                         NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                    EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                                                                                                                                                                                                                                                                                                                                                 ASTGASNONHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                    PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                          EBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                                                    WTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDNVMI TD
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2001US-0341117P.
2002US-0377066P.
2002US-03B6675P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 1.3
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No. 1.3e-235;
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30-APR-2004; 2004US-0567310P
03-JUN-2004; 2004US-0576501P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atherosclerosis; thrombosis; embolism; Parkinson congestive heart failure; cancer; inflammation; muscular dystrophy; diabetes; VP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crigler-Najjar syndrome; Gout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADV70294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mutated adence in an AAV virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arbetman AE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-2004; 2004WO-US019884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2004
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nemophilia; Pepck deficiency; galactosemia; phenylketonuria;
Origler-Najjar syndrome; Gout; Zellweger syndrome; ischemia;
atherosclerosis; thrombosis; embolism; Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virus (AAV) capsid protein that when present eased immunoreactivity to the virion as wild-type virion, useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ⋧
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Example 5 SEQ ID ö 20; 136pp; English.

CC protein that when present in an AAV virion imparts decreased continuous control to the virion as compared to the corresponding wild-type virion. Also described are: a polynucleotide encoding the mutated protein above; a recombinant AAV virion comprising the mutated protein above; and delivering a recombinant AAV virion to a cell or tissue of a vertebrate cut enterologous nucleic acid molecule to a cell or tissue of a vertebrate cubject, where the protein encoded by the heterologous nucleic acid molecule is expressed at a level that provides a non-primate, mammalian cubic acid molecule is expressed at a level that provides a non-primate, mammalian cubic acid molecule is expressed at a level that provides a non-primate, mammalian cubic acid molecule acid molecule encodes a therapeutic protein inparts decreased control elements capable of directing the in vivo transcription confined to control elements capable of directing the in vivo transcription is useful for treating or preventing a wide variety of disorders such as hemophilia, glycogen storage deficiency type 1A, Pepck deficiency. Capalactosemia, phenylketonuria, Crigaer-Najjar disease, Gout and Lesch-schemic, inflammatory and immune disorders, muscular dystrophies, and capables. This is the amino acid sequence of adeno-associated virus 1 capaid protein VPI. describes a mutated adeno-associated virus (AAV) capsid then present in an AAV virion imparts decreased

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-2003; 2003US-0508226P.
29-APR-2004; 2004US-0566546P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarthritic; neuroprotective; antiinflammatory; antidiabetic;
antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; anti-HIV;
virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005033321-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          colitis. The present sequence represents adeno-associated virus protein.
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                                                                                                                                                                                                                                                                                                                      WASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                                                                                                                                                  ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                                                                                                                                                                                MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                   NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                 EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                                                                                                                                                                                                               ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                                                                                                                                                                                                                                                                                                             736 AA;
   WTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                  LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                  NGSOAVGRSSFYCLEYFPSOMLRTGNNFTFSYTFEEVPFHSSYAHSOSLDRLMNPLIDQY
                                                                                                                                                                EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
                                 LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and cancer.
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                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENNSYLVANIA.
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                                                                                                                                                                                                                                                                                                                                                                            Score 2906; DB 9;
Pred. No. 1.3e-235;
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Query Match Best Local S Matches 533

Similarity

99.9%; 5c. 100.0%; Pr

Score 2902; DB 9; Pred. No. 2.8e-235;

Length Indels

735; 0

Gaps

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Mismatches

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The specification describes a method for lowering total cholesterol levels in a subject. The method comprises delivering to the subject a recombinant adeno-associated virus (AAV) comprising a gene encoding a human apolipoprotein E (apoE) or apoA under the control of a regulatory control sequence which directs expression of the gene. The recombinant AAV also comprises a capsid protein selected from an AAV serotype (e.g. AAV7 or AAV8) which preferentially expresses high levels of transgene in live. A therapeutically effective amount of apoE or apoA expression is obtained upon delivery of low dose of AAV. The method of the invention is useful for lowering total cholesterol levels in a subject, e.g. for treating atherosclerosis, and for correcting defects in lipoprotein. The present sequence represents a capsid protein of AAV serotype 1 (AAV1), which may be used in recombinant AAV vectors of the invention.
                                                                                                                                                                                                                                                                                     Lowering total cholesterol levels and treating atherosclerosis in subject comprises delivering a recombinant adeno-associated virus comprising an ANV servetype capsid protein or a gene encoding human apolipoprotein E (apoE) or apoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antilipemic; generapolipoprotein B; apoB; apolipoprotein lipoprotein defect; capsid protein.
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Sequence
                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-031700/03.
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New adeno-associated virus (AAV) clade comprising at least three AAV members, useful for preventing and/or treating arthritis, multiple
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29-APR-2004; 2004US-0566546P
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                                                                                 scleroderma,
                                                                  569pp;
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                                                                                 psoriasis,
                                                                                  hemophilia, HIV,
                                                                                  bacterial
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The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, asproidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.

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                                                                      PHTDGHFHPSPLMGGPGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                           PHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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                      IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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Pred. No. 1.9e-234;
0; Mismatches 2;
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XX ADZ27
XX 30-JU
DT 30-JU
XX XX Adenc
XX rheum
XW scler
KW bacte

30-JUN-2005

(first

entry.

ADZ27086

standard;

protein;

737

Adeno-associated virus

protein

SEQ

NO UI

rheumatoid arthritis; multiple sclerosis; sarcoidosis; diabetes; scleroderma; psoriasis; vasculitis; Crohn's disease; hemophilia; bacterial infection; cancer; ulcerative colitis; antirheumatic;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarthritic; neuroprotective; antiinflammatory; antiidabetic;
antipsoriatic; vasotropic; gastrointestinal-gen.; hemostatic; a
virucide; antibacterial; cytostatic; antiulcer; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New adeno-associated virus (AAV) clade comprising at least three members, useful for preventing and/or treating arthritis, multipl sclerosis, diabetes, scleroderma, psoriasis, hemophilia, HIV, bac
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29-APR-2004; 2004US-0566546P.
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EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                          EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                        WTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDNVMITD
                                                                                                                       WTGASKYNLNGRESI INPGTAMASHKDDEDKFFPMSGVMI FGKESAGASNTALDNVMITD
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Pred. No. 1.9e-234;
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WASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS á 밁 Ś 밁 5 밁 8 

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                                                                                                                                                                The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, sarcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
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   Claim 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an adeno-associated virus (AAV) clade comprising at least three AAV members, where each member of the AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05. The methods and compositions of the present invention are useful for the prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, arcoidosis, diabetes, scleroderma, psoriasis, vasculitis, Crohn's disease, hemophilia, HIV, bacterial infection, cancer and ulcerative colitis. The present sequence represents the amino acid sequence of an adeno-associated virus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 736 AA;
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                                                                                                                                               EBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                                                                                                                                                WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                      IEWBLQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                                                PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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99.1%;

 Mismatches

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ARBS9847;

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DT 28-MAR-2001 (first entry)

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DT 28-MAR-2001 (first entry)

XX

AV6; gene therapy; AAV viral vector; cystic fibrosis;

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ARW atherosclerosis; sickle cell anaemia; thalassaemia;

KW atherosclerosis; sickle cell anaemia; thalassaemia;

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ANV6

Adeno associated virus.

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cancer;

AIDS;

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Best Local Similarity
Matches 529; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to adeno-associated virus serotypes. The present sequence is capsid protein VPI of one such serotype (AAV6). AAV6 can be used to contruct AAV viral vectors for use in gene therapy for a range of disorders: cystic fibrosis, cancer, AIDS, atherosclerosis, sickle cell anaemia, thalassaemia, blood clotting disorders and diabetes. The AAV viral vectors have increased transduction efficiency of a particular host cell as the AAV virion containing the AAV vector genome can be modified to express a capsid protein of an AAV serotype that transduces the selected host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno-associated virus serotype 6 and viral vector derived from it gene therapy of cystic fibrosis, cancer, acquired immunodeficiency syndrome, sickle cell anemia, thalassemia and diabetes.
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 534
                                                                         PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
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Pred. No. 9.1e-234;
3; Mismatches 2;
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Search

completed: November 23,

2005, 17:35:14

Job time : 97.4286 secs



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	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	November 23, 2005, 17:29:19 ; Search time 18.8571 Seconds (without alignments) 2724.684 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-696-282-17 2906 1 MASGGGAPMADNNEGADGVGNNGLYTEPRPIGTRYLTRPL 534
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 segs, 96216763 residues
Total number of	Total number of hits satisfying chosen parameters: 283416
Minimum DB seq . Maximum DB seq .	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing: Minimum Match Maximum Match Listing first	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	PIR 80:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

	108.5	109	109	109	113.5	115.5	118	121	122.5	123.5	175	177.5	184	188	189	189	194	194	196.5	197	226	229	232.5	232.5	234.5	487.5	517	1676	2177.5	Score
	3.7	٦. 8	3.B	•		4.0	4.1	4.2	4.2	4.2	6.0	6.1	6.3	6.5	6.5	6.5	6.7	6.7	6.8	6.8	7.8	•	8.0	•	8.1	16.8	17.8	57.7	74.9	Match 1
1	1711	1186	1072	418	2817	345	739	635	880	690	722	702	748	737	727	584	727	722	718	716	722	587	729	729	723	781	673	732	504	Length I
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## ALIGNMENTS

cost protein - adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Species: adeno-associated virus type 2
C;Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 09-Jul-2004
C;Accession: A03698
R;Srivastava, A.; Lusby, E.W.; Berns, K.I.
J. Virol. 45, 555-564, 1983
A;Title: Nucleotide sequence and organization of the adeno-associated virus A;Reference number: A03694; MUID:83164299; PMID:6300419
A;Accession: A03698 RESULT 1 C; Superfamily: adeno-asso C; Keywords: coat protein A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-504 <SRI>
A;Residues: 1-504 <SRI>
A;Cross-references: UNIPROT:P03135; UNIPARC:UPI0000127C8E; EMBL:J01901; NID:g209616; PID
C;Superfamily: adeno-associated virus coat protein 밁 S S 밁 문 Ş 밁 ð 밁 δ 밁 ð 밁 Query Match Best Local S Matches 392 C Local 2 120 421 240 180 181 121 358 361 300 301 241 61 61 Similarity ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS EBEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFT NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTG WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD 74.9%; Score 2177.5; DB 1; llarity 82.5%; Pred. No. 1.4e-152; Conservative 33; Mismatches 47; Indels Length 504; 3; Gaps 475 180 240 179 119 120 60 420 357 360 299 300

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418

PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTG

472

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N; Alternate names: V
C; Species: muscovy c
C; Date: 19-Mar-1997
C; Accession: $52210
                                         RESULT
VCPVB5
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A;Residues: 1-732 <ZAD>
A;Residues: 1-732 <ZAD>
A;Cross-references: UNIPROT:Q83289; UNIPARC:UPI00000F6C5D; EMBL:X75093; NID:g609091;
A;Experimental source: strain FM
coat protein VP1 - bovine parvovirus N;Contains: coat protein VP2 C;Species: bovine parvovirus
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R;Zadori, Z.; Erdei, J.; Nagy, J.;
submitted to the EMBL Data Library,
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|Species: muscovy duck parvovirus
|Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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Best Local
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                                                                                                                                                                                                                                      GPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYS
                                                                                                                                                                                                                                                                           SDIMVTDEQEIAPTNGVGWRPYGLTVTNEQNTTTAPTNAELEVLGALPGWVWQNRDIYLQ
                                                                                                                                                                                                                                                                                          DNYMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQ
                                                                                                                                                                                                                                                                                                                                 ANWSIWSKGNKVFLKOREYLLQPGPVATTHTEDQASSVPAQNIIGIAKDPYRSGSTLAGI
                                                                                                                                                                                                                                                                                                                                                             NSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKE--SAGASNTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVITINDGVTTI ANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTNPDSN-TQYAGYSTPWGYFDFNRFHCHFSPRDWQRLINNHWGIRPKALKFKIFNVQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAEGGSGAMGDSAGGADGVGNASGNWHCDSQWLGDTVITKTTRTWVLPSYNNHMYQAITS
                                                                                                                                                                                TGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRP
                                                                                                                                                                                                                                                                                                                                                                                          DOYLWNFSEV-NGGRNAO----FKKAVKGAFGAMGRNWLPGPKLLDQRVRAYSGGTDNY
                                                                                                                                                                                                                                                                                                                                                                                                                     DQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTK--TDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNQSGARFNDRSAFYCLEYFPSQMLRTGNNFEFSFEFEEVPFHSMFAHSQDLDRLMNPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVTTQDQTKTIANNLTSTIQIFTDNEHQLPYVLGSATEGTMPPFPSDVYALPQYGYCTMH
                                                                                                                                                           TGQCTVEMVWELRKENSKRWNPEIQFTSNFGNRTSTMFAPNETGGYVEDRLIGTRYLTQN
                                                                                                                                                                                                                    GPIWAKIPKTDGKPHPSPNLGGFGLHNPPPQVFIKNTPVPADPPLEYVNQKWNSYITQYS
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                         R;Shade, R.O.; Blundell, M.C.; Cotmore, S.F.; Tattersall, P.; Astell, C.R. J. Virol. 58, 921-936, 1986
A;Title: Nucleotide sequence and genome organization of human parvovirus B19 isolated A;Reference number: A24299; MUID:86200451; PMID:3701931
A;Accession: A24299
                                                                                               C;Species: parvovirus B19
A;Note: host Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision
C;Accession: A24299
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 A; Molecule type: DNA
A; Residues: 1-781 <SHA>
                                                                                                                                                          coat protein VP1 - parvovirus B19
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28-Dec-1987 #text\_change

09-Jul-2004

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C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 0
C;Accession: A26104
R;Chen, K.C.; Shnl1, B.C.; Moses, E.A.; Lederman, M.; Stout, E.R.
J, Virol. 60, 1085-1097, 1986
A;Title: Complete nucleotide sequence and genome organization of
A;Reference number: A26104; MUID:87061184; PMID:3783814
A;Accession: A26104
A;Molecule type: DNA
A;Residues: 1-673 < CHB>
A;Cross-reference: UNIPACO:PO7297; UNIPARC:UPI0000127D77; EMBL:M
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GGAPMADNNEGADGYGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSASTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAHRQY-AITTPWSYFNFNQYSSHFSPNDWQHLVNDYERFRPKAMIVRVYNLQIKQIMT 280
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                                                                                                                                                                     MGGFGLKNPPPQILIK--NTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENS 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNPLIDQYLYYLNRTQN------QSGSAQNKDLLFSRGSP-----AGMSVQPKNWL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --NNGSOAVGRS-----SFYCLEYFPSOMLRTGNNFTFSYTFEEVPFHSSYAHSOSLDRL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGAMGTVYNNDLTAGMHIFCDGDHRYPYVQHPWDDQCMPELPNSIWELPQYAYIPAPISV 340
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                                                                                                                                                                                                                               HTFTREARTKLITGSNGADGDYKEWWMLPNQMWDSAPISRYNPIWVKVPRVNRKTLLDTQ 575
                                                                                                                                                                                                                                                                                     ERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSG 337
KNWRPEYMHS---ATNMSVDAYTINNAGVY
                                                   KRWNPEVQYTSNYAKSANVD-FTVDNNGLY
                                                                                                               DGSIPMSHPPGTIFIKLARIPVPGNGD-----
                                                                                                                                                                                                                                                                                                                                                                                                     VM-----IFGKE------SAGASNTALDNVMITDEEEIKATNPVAT 372
                                                                                                                                                                                                                                                                                                                                           VRAVRVGYSTDPIYGGQQPESDLLRLRYSASAAEGQQNPILEN-----
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25.1%;
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Pred. No. 4.4e-30;
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                                                                                                                  SFLNIYVIGOVSCEVVWEVEKRGT
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A;Cross-references: UNIPROT:P07299; UNIPARC:UPI0000127D7C; EMBL:M13178; NID:g333375; PID C;Superfamily: parvovirus coat protein C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                          coat protein VP1 - porcine parvovirus

N;Contains: coat protein VP2

C;Species: porcine parvovirus

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09

C;Accession: B33302

R;Ranz, A.I.; Manclus, J.J.; Diaz-Aroca, E.; Casal, J.I.

J. Gen. Virol. 70, 2541-2553, 1989

A;Title: Porcine parvovirus: DNA sequence and genome organization.

A;Reference number: A33302; MUID:90010964; PMID:2794971

A;Accession: B33302;
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A;Residues: 1-723 <RAN>
A;Crose-references: UNIPROT:P18546; UNIPARC:UPI0000174964;
C;Genetics:
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Matches 139
                                                                                                                                                               ;Superfamily: parvovirus coat protein
;Keywords: coat protein
;145-723/Product: coat protein VP2 #s
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                                                                                Similarity 23.:
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVKDVTDKTGGGV-QVTDSTTGRLCMLVDHEYKYPYVLGQGQDTLAPELPIWVYFPPQYA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEASTGAGGGGSNSVKSMWSEGATFSANSVTCTFSRQFLIPYDPEHHYKVFSPAASSCHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADNNEGADGVGNAS--GNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISSASTGASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPS-PLMGGFGLKNPPPQILIKNTPVPANP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGASNTALDNV-----MITDEEEIKATNPVATERFGTVAVNFOSSSTDPATGDVHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STKEGDSSNTGAGKALTGLSTGTSQNTRISLRPGPVSQPYHHWDTDKYVTGINAISHGQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASGKEAKVCTISPIMGYSTPWRYLDFNALNLFFSPLEFQHLIENYGSIAPDALTVTISEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-----NHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIGGIKSMGITTLVQYAVGIMTVTMTFKLGPRKATGRWNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLMVGSVWNRRALHYESQLWSKIPNLDDSFKTQFAALGGWGLHQPPPQIFLK--ILPQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYG---NAEDKEYQQGVGRFPNEKEQLKQLQGLNMHTY----FPNKGTQQYTDQIE-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVSKTKTDNNNSNFTWTGASKYNLNGRESIINPG-TAMASHKDDEDKFFPMSGVMIFGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQHFYEMYNPL---YGSRLGVPDTLGGDPKFRSL----THEDHAIQPQNFMPGPLVNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOSLDRLMNPLIDQYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGPCYRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLTVGDVNTQGISGDSKKLASEESAFYVLEHSSFQLLGTGGTASMSYKFPPVPPENLEGC
  SGGGGG-GGGGRGAGGVGVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                     SGGGAPMADNNEGADGVGNASGNWH--CDSTWLGD---RVITTSTRTWALPTYNNHLYKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAEFSATKFASFITQYSTGQVSVEIEWEL-QKENSKRWNPE 496
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                                                                                                                                                                 protein VP2 #status predicted
                                                                                                    8.1%; Score 234.5; DB 1; 23.2%; Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 487.5; DB 1; 27.4%; Pred. No. 8.3e-28; tive 84; Mismatches 239;
                                                                                  Mismatches 241;
                                                                                                                                                                   <VP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  coat protein VP1 - porcine parvovirus (strain 90HS)

N; Contains: coat protein VP2
C; Species: porcine parvovirus
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-0000;
C; Accession: A60006
R; Sakurai, M: Nishimori, T: Ushimi, C: Nakajima, H.
Virus Res. 13, 79-86, 1989
A; Title: Nucleotide sequence of capsid protein gene of porcine parvo A; Reference number: A60006; MUID:89319168; PMID:2750278
A; Residues: 1-729 <SAKS
A; Residues: 1-729 <SAKS
A; Residues: 1-729 <SAKS
                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P33484; UNIPARC:UPI0000127C6E C;Superfamily: parvovirus coat protein C;Keywords: coat protein; glycoprotein C;Keywords: coat protein; glycoprotein F;151-729/Product: coat protein VP2 #status predicted <VP2>F;172,198,282,330,433,471,573,604,651/Binding site: carbohy
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                                         112 FKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADV
                                                                                                                                                                       174
                                                                                                                                                                                                                                                        137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLQGPIWAKIPHTD--GHFHPSPLMGGFGLK-NPPPQILIKNTPVPANPPAEFSA-TKFA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P--GTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD---NVMITDEEEIK--ATNP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I----SSASTGAS-NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLN
    QEIFNVVLKTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLP
                                                                                     IHVLNSESGVAGQMVQDDAHTQMVTPWSLIDANAWGVWPNPADWQLISNNMTEINLVSFE
                                                                                                                                                                     SGGGGG-GGGGRGAGGVGVSTGSFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                                                                                                                                                                                        SGGGAPMADNNEGADGVGNASGNWH---CDSTWLGD---RVITTSTRTWALPTYNNHLYKQ
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                                                                                                                            IS--SASTGAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLN 111
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                          8.0%;
                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                      Score 232.5; DB 1;
Pred. No. 4.5e-09;
6; Mismatches 245;
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526 657

706

603 410 543

(covalent) #stati

168

292

57

31

232

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RESULT 7

VCPVNA

VCPVNA

COAT protein VP1 - porcine parvovirus (strain N;Contains; coat protein VP2

C;Species: porcine parvovirus

C;Species: porcine parvovirus

C;Date; 31-Dec-1990 #sequence revision 31-Dec-
C;Date; 31-Dec-1990 #sequence contains

C;Accession: B33743; D48472

C;Accession: B33743; D48472

C;Accession: B33743; D48472
                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bergeron, J.; Menezes, J.; Tijssen, P. Virology 197, 86-98, 1993
A;Title: Genomic organization and mapping of transcription A;Reference number: A48472; MUID:94025614; PMID:8212598
A;Accession: D48472
밁
                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 11-729 <BRP>
A;Cross-references: UNIPARC:UPI0000174965
A;Experimental source: NADL-2, ATCC VR-742
A;Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBIP:138794)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-729 < VAS>
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                                                                                                                                                                                                                               Superfamily: parvovirus coat protein ;Superfamily: parvovirus coat protein ;Reywords: coat protein PD2 #status predicted . ;151-729/Product: coat protein PD2 #status predicted . ;32,172,198,282,330,433,471,573,604,651/Binding site:
                                                                                                                                                                         Query Match
Best Local :
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  233
                                    58
                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APKQQFNQQAPLNLENTNNGTLLPSDPIGGKPNMHFMNTLNTYGPLTALNNTAPVFPNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIVPTADTQYNDDE----PNGAIRFTMGYQHGQLTTS-----SQELERYTFNPQSKCGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGIYHFDTKPL--KLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VATERFGTVA-VNFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDVYLQGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLLFSRGSPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIIN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TFSYTFEEVPFHSSYAHSQSLDR-----LMNPLI--DQYLYYLNRTQNQSGSAQNK 257
  IHVLNSESGVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFE
                                                                            SGGGGG-GGGGRGAGGVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKR
                                                                                                              SGGGAPMADNNEGADGVGNASG--NWHCDSTWLGD---RVITTSTRTWALPTYNNHLYKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSNFWWKGTLTFTAKMRSSNMWNPIQQHTT-----TAENIGNYI-PTNIG
                                  IS--SASTGAS----NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLN
                                                                                                                                                         Conservative
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                                                                                                                                                       85;
                                                                                                                                                       Score 232.5; DB 1;
Pred. No. 4.5e-09;
5; Mismatches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-Dec-1990 #text_change
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A;Title: The complete nucleotide sequence of parvovirus A;Reference number: A44276; MUID:93297126; PMID:8517025 A;Accession: B44276
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coat protein VP1 - parvovirus LuIII
(;Species: parvovirus LuIII
(;Spate: 17-Reb-1994 #sequence_revision
(;Accession: B44276
R;Diffoot, N.; Chen, K.C.; Bates, R.C.;
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B44276
                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-587 <DIF>
A;Residues: 1-587 <DIF>
A;Cross-references: UNIPROT:P36310; UNIPARC:UPI0000127D7E; GB:M8188
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein; glycoprotein
C;Keywords: coat protein; glycoprotein
E;49,90,220,304,371,503,511,514,539,571/Binding site: carbohydrate
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                      203
                                                                                                                                                                           84 VRVHNTNDTGTASHMAMDDAHEQIW-TPWSLVDANAWGVWFQPSDWQYISNNMIHINLHS
                                                                                                                                                                                                               53 --- HLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKR
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                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                LNEKLENIQVKBYT-TNDGYTTIA---NNLTSTVQVFSDSEYQLPYVLGSAHQGCL----
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                    WKPTIPSPYRYYFSCDRNLSVTYKDEAGTITDTMGLASGLNSQFFTIENTQRINLLRTGD
                                                          --PPFPA-----
                                                                                                                                                                                                                                                   -----VATERFGTVA-VNFQSSS-----TDPATG--DVHAMGALP-----GMVWQDRDV
                                                                                              LDQELFNVVIKTYTEQNTGAEAIKVYNNDLTAAMWVALDSNNILPYTPAIDNQETLGFYP
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                7.9%;
22.7%;
                                                        ----DVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPS-QMLRTGN 206
                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                    Score 229; DB 1;
Pred. No. 5.9e-09;
                                                                                                                                                                                                                                                                                                                                  Mismatches 228;
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Coat protein VP1 - parvovirus H1
C.Species: parvovirus H1
A;Note: host Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Ju1-2004
C;Accession: A03699
R;Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A;Title: Parvovirus genome: nuclectide sequence of H-1 and mapping of its genes A;Reference number: A03695; MUID:83112183; PMID:6823009
A;Accession: A03699
A;Accession: A03699
A;Molecule type: DNA
A;Residues: 1-722 <RHO>
A;Cross-references: UNIPROT:P03136; UNIPARC:UPI0000127D7D; EMBL:X01457; EMBL:JO:C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NF-TFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQ------YLYYLNRTQN-
                                                                                                                                                                                                                                                                                                                                            RPKRLNFKLFNIQVKEVTT-----NDGVTTIANNLTSTVQVFSDSEYQLFYVLGSAHQGC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GASNTALDNVMITDEEEIKATNPVATER---FGTVAVNFQS--SSTDPATGDVHAMGALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQSWASQNNKDRYTW-DAVNYD-SGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSKTKTDNINSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDVTEATRVRPAQVGFCQPHDNFETSRAGPFKVPVVPADITQGLDHDANGSLRYTYDKQH
                                                                                                                                                                                                                                                                                                                                                                                                       RVTVHNNQTTGHGTKVKGNMAYDTHQQIW-TPWSLVDANAWGVWFQPSDWQFIQNSMESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGGGAPMADNNEGADGVGNASGNWHCDSTW--LGDRVITTSTRTWAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTP--VPANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WTNNCFIQSVPFTSEPN---ANQILTNRDNLAGKTDIHFTNAFNSYGPLTAFPH-----
                                                                                                                                                                                                                                                                                                                        NLDSLSQELFNVVVKTVTEQQGAGQDAIKVYNNDLTACMMVALDSNNILPYTPAAQTSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- PTYNNHLYKQISSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADGGGS-SGGGGGGGGGTGVSTGTYDNQTTYKFLGDGWVEITAHASRLLHLGMPPSENYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNSSNLSRIVTYGTFFWKGKLTLKAK---MRPNA-TWNPVFQISA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PAPIYPOGOIWDKELDLEHKPRLHTQAPFV---CKNNAPGOLLVRLAPNLTDQYD
TKTDNNNSNFTWTGASKYNLNGR--ESIINPGTA-----MASHKDDEDKFFPMSG
                                                                                                                                                 TLLRTGDEFTTGTYIFNTDPLKLTHTWQTNRHLACLQGITDLPTSDTATASLTANGDRFG
                                                                                                                                                                                          QMLRTGNNFTF-SYTFEEVPFHSSYA----HSQSLDRLMN-PLIDQYLYYLNRTQNQSG
                                                                                                                                                                                                                                                                            L-----PPFPAD---VFMIPQYGYLTLNNGSQ-----AVG----RSSFYCLE-YFPS
                                                               STQTQNVNYVTEALRTRPAQIGFMQPHDNFEANRGGPFKVPVVP---
                                                                                                         SAQNKDLLF--
                                                                                                                                                                                                                                      LGFYPWKPTAPAPYRYYFFMPRQLSVTSSNSAEGTQITDTIGEPQALNSQFFTIENTLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----QSGSAQNKD-LLFSRGSPAGMSVQPKNWLPG------PCYRQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 226; DB 1; I
Pred. No. 1.3e-08;
3; Mismatches 234;
                                                                                                       SRGSPAGMSVQPKNWLPGPCYRQQRVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 146;
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A;Residues: 1-716 <AST>
A;Residues: 1-716 <AST>
A;Cross-references: UNIPROT:P03137; UNIPARC:UPI0000127D6D; EMBL:V01115
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coat protein VP1 - minute virus of mice C;Species: minute virus of mice, murine parvovirus C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 C;Accession: A03700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
VCPV2M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 11, 999-1018, 1983
A;Title: The complete DNA sequence of minute virus of mice, A;Reference number: A03696; MUID:83143341; PMID:6298737
A;Accession: A03700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Astell, C.R.; Thomson, M.; Merchlinsky, M.; Ward,
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Best Local S
Matches 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498
                                                                                                                                                                                                                                                                                                        442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 KPTIASPYRYYFCVDRDLSVTYENQEGTVEHNVMGTPKGIPQFFTIENTQQITLLRTGDE
          455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 IRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---RVITTSTRTWALPTYNNHLYKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGEDHDAN----GAIRFNYGKQHGEDWAKQGAAPERYTWDAIDSAAGRDTARCFV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANPPAEF -- SATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVFMIPQYGY-----LTLNNGSQAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGG-----GSGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCR 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGALPGMVWQDRDVYLQGPIWAK----IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VMIFGKESAGASNTALDNVMITDEEEIKA-TNPVATERFGTVAVNFQSSSTDPATGDVHA
      NPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVD
                                                                                          LPGMVWQDRDVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTP--VPA
                                                                                                                                                                               GKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFOS--SSTDPATGDVHAMGA
                                                                                                                                                                                                                       GSVRYSYGKOHGENWASHGPAPERYTWDETSFGSGRDTKDGFIQSAPLVVPPPLNGI---
                                                                                                                                                                                                                                                               WTGASKYNLNGRESIINPG-----TAMASHKDDEDKFF-----PMSGVMIF
                                                                                                                                                                                                                                                                                                        SRHGTTQMGVNWVSEAIRTRPAQVGFCQPHNDFEASRAGP-FAAPKVPADITQGVDKEAN
                                                                                                                                                                                                                                                                                                                                                  SPAGMSVQPKNWL - - -
                                                                                                                                                                                                                                                                                                                                                                                            FATGTYYFDTNSV--KLTHTWQTNRQLGQPPLLSTF----PEADTDAGT-----LTAQG
                                                                                                                                                                                                                                                                                                                                                                                                                               F-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQEIFNVVLKTVTEQDLGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%;
ilarity 20.0%;
Conservative 88
                                                  ---PSPVYPQGQIWDKELDLEHKPRLHITAPFV---CKNNAPGQMLVRLGPNLTDQ
                                                                                                                                      -----LTNANPIGTKN----DIHFSNVFNSYGPLTAFSH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - IYPNGQIWDKELDLEHKPRLHVTAPFV---CKNNPPGQLFVHLGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 197; DB 1;
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                    ----PGPCYRQQRVSKTKTDNNNSNFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GRSSFYCLEYFPS-QMLRTGNN
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coat protein VP1 - minute virus of mice (strain MVMi)
(;Species: minute virus of mice, murine parvovirus
(;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 09-Ju1-2004
(;Accession: B23008; B29510
R;Sahli, R.; McMaster, G.K.; Hirt, B.
Rucleic Acids Res. 13, 3617-3633, 1985
Rucleic Acids Res. 13, 3617-3633, 1985
A;Reference number: A23008; MUID:85242059; PMID:3855242
A;Accession: B23008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-143; A; 145-718 < AST>
A; Cross-references: UNIPARC: UPI0000127D6C;
C; Superfamily: parvovirus coat protein
C; Keywords: coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P07302; UNIPARC:UPI0000174963; EMBL:X02481; R;Astell, C.R.; Gardiner, E.M.; Tattersall, P.
J. Virol. 57, 656-669, 1986
A;Title: DNA sequence of the lymphotropic variant of minute virus of mic A;Reference number: A29510; MUID:86115415; PMID:3502703
A;Accession: B29510
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VCPVIM
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Best Local Simi
Matches 122;
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    592
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                                         409 DVYLQGPIWAK---IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTP--VPANPPAEFSAT
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                                                                                                                                                                                                                                                                                              GSPAGMSVQPKNWL-----
                                                                                                                                                                                                                                                                                                                                                                               NF-TFSYTFEEVPFHSSYAHSQSLDRLMN--PLIDQYLYYLNRTQNQSGSAQNKDLLFSR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQBIFNVVLKTVTEQDSGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFKLFNIQVKEVTTND----GVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGG-----GSGGGGVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGGAPMADNNEGADGVGNASGNWHCDS--TWLGD---RVITTSTRTWALPTYNNHLYKQ
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PYYPQGQIWDKELDLEHKPRLHITAPFV----CKNNAPGQMLVRLGPNLTDQYDPNGATLS
                                                                                                                                                                                                                                                                                                                                        EFATGTYYFDTNPV--KLTHTWQTNRQLGQPPLLSTF----PEADTDAGT-----LTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVFMIPQYGY-----
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                                                                                                                           TALDNVMITDEEEIKATNPVATERFGTVAVNFQS--SSTDPATGDVHAMGALPGMVWQDR 408
                                                                                                                                                                                                              TWTGASKYNLNGRESIINPGTAMASHKDDEDKF-----FPMSGVMIFGKESAGASN
                                                                                                                                                                                                                                                     GSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGP-FAAPKVPADVTQGVDREA
                                                                                                                                                                                                                                                                                                                                                                                                                          KPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRL
                                                                                                                                                                     NGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILT
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20.5%; pred
20.5%; 82;
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Pred. No. 2e-06;
32; Mismatches 243;
                                                                                                                                                                                                                                                                                            ------PGPCYRQQRVSKTKTDNNNSNF
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J. Gen. Virol. 72, 867-875, 1991
A;Title: Construction and nucleotide sequence analysis of an infectious DNA clone.
A;Reference number: A38350; MUID:91202123; PMID:2016597
A;Accession: B38350
A;Molecule type: DNA
A;Residues: 1-722 <KAR>
A;Residues: 1-722 <KAR>
A;Cross-references: UNIPROT:P27437; UNIPARC:UPI0000174967; GB:D00765
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status predicted <VP2>
F;139-722/Product: coat protein VP2 #status predicted <VP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                     TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN---
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                                                               QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                                                                                             RGGAQTDENQAADGDPR - - -
                                                                                                                                                 FHPSPLMGGFGLK-----
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                                                                                                                                                                                                                                                                             ----IAHQDT------GRYPAGDWIQNINFNLPVTNDNVLLP
                                                                                                        -LKPRLHVNAPFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSR----IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LMNPLIDOYL--YYLNRTQNQS------
                                                                                                                                                                                                                                                                                                                                                             ----YAFGRQHGQKTTTTGETPERFTY-----
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A;Molecule type: DNA
A;Residues: 1-727 <CAR>
A;Residues: 10-727 <CAR>
A;Crose-references: UNIPROT:P04864; UNIPARC: C;Genetics:
A;Introns: 11/1
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
C;Keywords: coat protein VP2 #status
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A;Title: Cloning and sequence of DNA encoding structural A;Reference number: A03697; MUID:85265017; PMID:2991581
A;Accession: A03701
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c;Species: feline panleukopenia virus,
C;Date: 30-Jun-1987 #sequence_revision
C;Accession: A03701
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Best Local Similarity
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                                                                                                                                                                                                                                                         TNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGH
                                                                                                                                                                                                                                                                                           ----IAHQDT---
                                                                                                                                                                                                                                                                                                                                                            RGGAQTDENQAADGDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                TNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKIPIAAG
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                                                                                      TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN---
                                                                                                                      QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                        FHPSPLMGGFGLK-----
                                                                                                                                                                                                                                                                                                                           NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SFYCLE-YFPSQMLRTGNNF---TF-----SYTFEE-----VPFHSSYAHSQSL
                                                                                                                                                                                                                                                                                                                                                                                            -GSAQNKDLLFSRGSPAGMSVQPKNWLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY
     VP2
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     canine
                                                                                                                                                                                                                         -GKTGINY--TNIFNTYGPLTALNNVP----PVYPNGQIWDKEFDTD--
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                                                                                                                                                      - LKPRLHVNAPFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSR----- IV
   parvovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PPFPA-----DVFMIPQYGYLTLNNGSQAVGRS------
                                                                                                                                                                                        -----NPPPQILIKNTPVPAN---PPAEFSATKFASFIT
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coat protein VP1 - feline panleukopenia virus N;Contains: coat protein VP2 C;Species: feline panleukopenia virus, FPLV C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-C;Accession: B36608 R;Marryn, J.C.; Davidson, B.E.; Studdert, M.J. Gen. Virol. 71, 2747-2753, 1990

31-Dec-1991

#text\_change

09-Jul-2004

(strain

193

A;Title: Nucleotide sequence of feline panleukopenia virus: A;Reference number: A36608; MUID:91073139; PMID:2174965

comparison

with

canine

parv

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submitted to the EMBL Data Library, November 1994 A;Description: Polish isolates of canine parvovir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: canine parvovirus
C;Date: 05-Mar-1995 #sequenc
C;Accession: S49594
R;Mizak, B.; Plucienniczak,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: UNIPROT: Q66208; UNIPARC: UPI00000FA046; EMBL: Z46651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-584 < MIZ>
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Similarity 20.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---HL-----YKQI-----SSASTGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW
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                           KRWNPEVOYTSNYAKSANVDFTVDNNGLYTEPRPIG
                                                                                                                                                                                                                                                                                     SK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSH----TGTSGTPTNIYHGTDPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRLINNNWGFRPKRLNFKLFNIQVKEVT---TNDGVTTIANNLTSTVQVFSDSEYQLPYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGQP-AVRNERATGSGNGSGGGGGGGS--GGVGISTGTFNNQTEFKFLENGWVEITANSS
                                                           PFVCQNNCPGQLFVKVAPNLTNEYDPDASANMSR---
                                                                                        ----NPPPQILIKNTPVPAN----PPAEFSATKFASFITQYSTGQVSVEIEWELQKENS
                                                                                                                          IFNTYGPLTALNNVP-----PVYPNGQIWDKEFDTD----
                                                                                                                                                      TDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLK------
                                                                                                                                                                                                                      DEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSS
                                                                                                                                                                                                                                                    TQGPFKTPIAAGRGGAQTDENQAA----DGDPRYAFGRQHGQKTTTTGETPERFTYIAHQD
                                                                                                                                                                                                                                                                                                                  SEGGTNFGYIGVQQDKRRGVTQMGNTNYITEATIMRPAEVGYS
                                                                                                                                                                                                                                                                                                                                                TQNQS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLI VNTMSELHLVSFEQEI FNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFT
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                                                                                                                                                                                                                                                                                   ----TKTDNNNSNFTWTGASKY---NLNGRESIINPGT----AMASHKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSAQNK-------DLLFSRGSPAGMSVQPKNWLPGPCYRQQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coat protein
                                                                                                                                                                                     -GRYPEGDWIQNINFNLPVTDDNVLLPTDPIG----GKTGINY--TN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 189; DB 2;
Pred. No. 5.2e-06;
9; Mismatches 223
VDNOFNYV-PSNIG
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A;Accession: B36608
A;Molecule type: DNA
A;Residues: 1-727 <MAR>
A;Residues: 1-727 <MAR>
A;Cross-references: UNIPROT:P24840; UNIPARC:UPI0000127D56; GB:X55115
C;Superfamily: parvovirus coat protein
C;Keywords: coat protein
F;144-727/Product: coat protein VP2 #status predicted <VP2>
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Matches 135; Conserv
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TYSDFWWKGKLVFKAKLRASHTWNPIQQMSIN-----
                          QYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIG 526
                                                         FHPSPLMGGFGLK-----NPPPQILIKNTPVPAN---PPAEFSATKFASFIT
                                                                                                                    TDPIG----GKTGINY--TNIFNTYGPLTALNNVP------PVYPNGQIWDKEFDTD--
                                                                                                                                              INPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGH 426
                                                                                                                                                                           ------IAHQDT------GRYPEGDWIQNINFNLPVTNDNVLLP
                                                                                                                                                                                                       NLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALD-NVMITDEEEIKA 366
                                                                                                                                                                                                                                         RGGAQTDENQAADGDPR------YAFGRQHGQKTTTTGETPERFTY-----
                                                                                                                                                                                                                                                                   -GSAQNKDLLFSRGSPAGMSVQPKNWLPGPCY---RQQRVSKTKTDNNNSNFTWTGASKY
                                                                                                                                                                                                                                                                                                 TNFGDIGVQQDKRRGVTQMGNTDYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 189; DB 1; Length 72
20.6%; Pred. No. 7.2e-06;
ative 73; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                             -----LMNPLIDQYL--YYLNRTQNQS------
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--VDNQFNYV-PNNIG
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Search completed: November 23, 2005, 17:44:04 Job time: 20.8571 secs

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Perfect score:
Sequence:
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    pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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tissues.";
J. Virol. 78:6381-6388(2004).

EMBL; AX530607; AA839292.1; -; Genomic_DNA.

SMR; Q6JC12; 217-736.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0019028; F:structural molecule activity; IE
InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 736 AA; 81364 MW; F2D75A06662E6376 CR
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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NCBI_TaxID=272636;
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EMBL; AY530611; AAS99296.1; -; Genomic_DNA.

SMR; Q6JC08; 217-736.

G0; G0:0019028; C:viral capsid; IEA.

G0; G0:0019028; F:structural molecule activity;

InterPro; IRR001403; Parvo_coat.

Pfam: PF00740; Parvo_coat: 1.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
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SEQUENCE 736 AA; 81317 MW;
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X MEDINE=98080418; PubMed=9420229;

X MEDINE=98080418; PubMed=9420229;

X Rutledge E.A., Halbert C.L., Russell D.W.;

XT "Infectious clones and vectors derived from adeno-associated virial capture of their than AAV type 2.";

XT (AAV) serotypes other than AAV type 2.";

XT (AAV) serotypes other than AAV type 2.";

RI J. Virol. 72:309-319(1998)

DR GAR; OS6137; 217-736.

DR SMR; OS6137; 217-736.

DR SMR; OS6137; 217-736.

DR GO; GO:00019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0019028; F:structural molecule activity; IEA.

DR InterPro; IPR001403; Parvo_coat.

DR Pfam; PF00740; Parvo_coat.

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01-MAR-2004 (TrEMBLrel. 2
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Adeno-associated virus 6.
Viruses; ssDNA viruses; FNCBI TaxID=68558;
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Pred. No. 5e-2
3; Mismatches
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RESULT 5 Q6JC13\_9VIRU

(TrEMBLrel. 27, (TrEMBLrel. 27, PRELIMINARY;

Created) Last seq

sequence update)

PRT;

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Query Match
Best Local Similarity
Matches 530; Conserv
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Q6JC13;
Q6JC13;
Q5_JUL-2004 (TrEMBLrel. 27,
05_JUL-2004 (TrEMBLrel. 27,
05_JUL-2004 (TrEMBLrel. 27,
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J. Virol. 78.6381-6388(2004).

EMBL; AY530606; AAS99291.1; -; Genomic_DNA.

SMR; O6JC13; 218-737.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; F:structural molecule activity;
InterPro; IPR001403; Parvo coat.
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SEQUENCE
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PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
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AA; 81332 MW;
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Pred. No. 6e-202;
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annotation
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.R., Lu Y., Calcedo
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O5-JUL-2004 (TrEMBLrel. 27,
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Capsid protein VP1.
Name=cap;
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Wilson J.
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tissues";
J. Virol. 78:6381-6388(2004).
EMBL; AY530609; AAS99294.1; -
SMR; C6JC10; 217-736.
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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mes 528; Conserv
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GO:0005198; F:structural molecule activity;
erPro; IPR001403; Parvo_coat.
m; PF00740; Parvo_coat; 1.
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Pred. No. 1.7e-200;
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RESULT 8
Q670Q8_9VIRU
ID Q670Q8;
AC Q670Q8;
DT 25-CCT-2004 (T
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DT 25-CCT-2004 (T
DT 25-CCT-2005;
Capaid protein
GN Name=cap;
OS Adeno-associat
OC Viruses; saDNA
OX NCBI_TaxID=272
RN [1]
RP NUCLEOTIDE SEQ
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EMBL; AY530585; AAS99270.1; -; Gen
SMR; O6JC34; 217-735.

GO; GO:0005198; F:structural molec
InterPro; IPR001403; Parvo coat.
Pfam; PF00740; Parvo coat; 1.
SEQUENCE 735 AA; 81962 MW; 85D
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PubMed=15.63731; DOI=10.1128/JVI.78.12.6381-6388.2004;

Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo Wilson J.M.;
                   Adeno-associated virus. Viruses; ssDNA viruses; NCBI_TaxID=272636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Clades of Adeno-associated viruses are widely tissues.";
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NCBI_TaxID=272636;
[1]
                                                      Capsid protein Name=cap;
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; Pred. No. 1.3e.
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O6JC28 9VIRU

O6JC28;
O5-JUL-2004 (;
O5-JUL-2004 (;
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O5-JUL-2004 (;
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SMR; Q67008; 217-735.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0005198; F:structural molecule activity; IEA.
InterPro; IPR001403; Parvo_coat.
Pfam; pF000740; Parvo_coat; 1.
SEQUENCE 735 AA; 81887 MW; 258BFB955F1C9925 CRC64;
                                                                                Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
                                  NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
Wilson J.M.;
 "Clades of Adeno-associated viruses tissues.";
J. Virol. 78:6381-6388(2004).
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4 (TrEMBLrel.
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                                                                                                Parvoviridae;
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; Pred. No. 1.5e
34; Mismatches
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Gao G., Van Wilson J.M. "Clades of

Adeno-associated

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tissues.";

J. Virol. 78:6381-6388(2004).

EMBL; AY530622; AAS99307.1; -; Genor

SMR; Q6JBZ7; 217-735.

GO; GO:0019028; C:viral capsid; IEA

GO; GO:0005198; F:structural molecu.

Genomic

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Viruses; ssDNA viruses;
NCBI_TaxID=272636;
[1]
                                                                                                                                            NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.
Gao G., Vandenberghe L.H., Alvira M.
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G0:0019028; C:viral capsid; IEA.
G0:0005198; F:structural molecul
cerPro; IPR001403; Parvo_coat.
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pr00740; Parvo_coat; 1.
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                                                            NUCLEOTIDE SEQUENCE.

WEDLINE=98080418; PubMed=9420229;
Rutledge E.A., Halbert C.L., Russell D.W.;
"Infectious clones and vectors derived from adeno-
(AAV) serotypes other than AAV type 2.";
J. Virol. 72:309-319(1998).

EMBL; AP028705; AAB95452.1; -; Genomic_DNA.
SMR; O56139; 217-736.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; P:structural molecule activity; IE
InterPro; IPR001403; Parvo_coat.
Pfam; PF00740; Parvo_coat.
SEQUENCE 736 AA; 81906 MW; DD52331AD5F0D70F CR
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Pfam; PF00740;
SEQUENCE 735
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056139_9VIRU PRELIMINARY;
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01-JUN-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Viruses; ssDNA viruses;
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0740; Parvo_coat; 1.
735 AA; 81947 MW; E
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84.8%; Pred. No. 3.66
87.1%;
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2530; DB 2;
No. 3.9e-176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                                                                                                          LYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSLQARNWLFGPCYRQQRLSKTANDNNNSNF
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                                                                                                                                                                                                                                                                                                                                EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN
 EIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
              EIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                              IPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSV
                                                                                                    DEEEIRTINPVATEQYGTVANNLQSSNTAPTTRTVNDQGALPGMVWQDRDVYLQGPIWAK
                                                                                                                      DEEBIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVMQDRDVYLQGPIWAK
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                                                   I PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSV
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Best Local S
Matches 454
                                                                         Pfam; PFO
SEQUENCE
                                                                                                                                                                                                                                  Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI TaxID=272636;
                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                             EMBL; AY530628; AAS99313.1; -; SMR; Q6JBZ1; 217-735.
                                                                                                                                                            "Clades of Adeno-associated viruses are tissues.";
                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                     Name=cap
                                                                                                                                                                                                                                                                               Capsid protein VP1
                                                                                                                                                                                                                                                                                                                         Q6JBZ1_9VIRU
Q6JBZ1;
                                                                                                                                                   J. Virol. 78:6381-6388(2004).
                                                                                                                                                                                  Wilson J.
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                                                                       GO:0019028; C:viral capsid; IEA. GO:0005198; F:structural molecule erPro; IPR001403; Parvo_coat. m; PP00740; Parvo_coat; 1. GEORGE 735 AA; 61868 MW; 1654ED6
                               al Similarity
454; Conserv
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MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                Conservative
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                                         87.0%;
85.0%;
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                               Score 2529.5;
Pred. No. 4.2e
34; Mismatches
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Last annotation update)
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                                                                                                         activity;
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Q65311;
Q1-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
01-NOV-1996 (TrEMBLrel. (
                                                                                                                                                                                                                                                     Virology 221:208-217(1996).

EMBL; U49704; AAC55049.1; -; Genomic_DNA.

SMR; Q65311; 217-736.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR001403; Parvo_coat.

Pfam; PF00740; Parvo_coat; 1.

SEQUENCE 736 AA; B1660 MW; AFF1EF47B5C67A10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96266430; PubMed=8661429; DOI=10.1006/viro.1996.0367; Muramatsu S., Mizukami H., Young N.S., Brown K.E.; "Nucleotide sequencing and generation of an infectious clone associated virus 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
STRAIN=3H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adeno-associated virus Viruses; ssDNA viruses;
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                                                                                    MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
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(TrEMBLrel.
                                                                                                                                                                      Conservative
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                                                                                                                                                                                            87.0%;
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; Parvoviridae;
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Last sequence update)
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                                                                                                                                                                        Score 2528; DB 2;
Pred. No. 5.5e-176;
8; Mismatches 46;
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Best Local S
Matches 453
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QGJC38;
QGJC38;
Q5_JUL-2004 (TrEMBLrel. 27,
05_JUL-2004 (TrEMBLrel. 27,
05_JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                               J. virol. 78:6381-6388(2004).

EMBL, AY530581; AA599266.1; -; Genomic SMR; O6JC38; 217-735.

GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule InterPro; IRR001403; Parvo coat.
                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
PubMed=15163731; DOI=10.1128/JVI.78.N.R., Lu Y., Calcedo
                                                                                                                                                                                                                                                                                                               Adeno-associated virus.
Viruses; ssDNA viruses;
NCBI_TaxID=272636;
                                                                                                                                                                                                                                                                                                                                                 Capsid protein Name=cap;
                                                                                                                                                              Pfam; PF00740;
SEQUENCE 735
                                                                                                                                                                                                                                            tissues.";
                                                                                                                                                                                                                                                                 Wilson J.M.
                                                                                                                                                                                                                                                         "Clades of Adeno-associated viruses are
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                                                                               203 MATGSGAPVADNNEGADGVGNSSGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                        453;
                                                             61
                                                                                                                                  Similarity
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EVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLN 180
                                       MASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWALPTYNNHLYKQISS
                                                                                                                       Conservative
                                                                                                                                                              Parvo coat; 1.
AA; 81913 MW;
                                                                                                                                 86.9%;
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27,
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                                                                                                                                                                                                                                                                                                                              Parvoviridae;
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Last annotation update)
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                                                                                                                      Score 2524.5; DB 2;
Pred. No. 9.8e-176;
4; Mismatches 46;
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                                                                                                                                                                                              activity;
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Capsid protein VP1.

GN
Name=cap;
Adeno-associated viruses; Parv
OX
Viruses; SSDNA viruses; Parv
OX
NCBI_TAXID=272636;
RN
(1)
AC
RP
NUCLEOTIDE SEQUENCE.
RN
PubMed=15163731; DOI=10.1128
RA
Gao G., Vandenberghe L.H., P
RA
Wilson J.M.;
RA
Gao G., Vandenberghe L.H., P
RA
Wilson J.M.;
Clades of Adeno-associated
RT
Clades of Adeno-associated
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Clades of Adeno-associated
RL
J. Virol. 78:6381-6388(2004)
DR
EMBL; AV530577; AAS99262.1;
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A Wilson J.M.;

AT "Clades of Adeno-associated viruses are widely disseminated in human tissues.";

RT J. Virol. 78:6381-6388(2004).

DR EMBL; AY530577; AAS99262.1; -; Genomic_DNA.

DR SMR; Q6UC42; 217-735.

DR GO; GO:0019028; C:viral capsid; IEA.

DR GO; GO:0019028; C:viral molecule activity; IEA.

DR GO; GO:001318; F:structural molecule activity; IEA.

DR InterPro; IPR001403; Parvo_coat.

DR Pfam; PF00740; Parvo_coat; 1.

SQ SEQUENCE 735 AA; 82114 MM; 59E748255744D5FB CRC64;
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Best Local Simi
Matches 453;
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PubMed=15163731; DOI=10.1128/JVI.78.12.6381-6388.2004;
Gao G., Vandenberghe L.H., Alvira M.R., Lu Y., Calcedo
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                                                                                                     I EWELOKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL
                         NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY
NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 86.9%; Score 2524.5; DB 2; Length
84.8%; Pred. No. 9.8e-176;
Ltive 35; Mismatches 45; Indels
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Search completed: November 23, Job time: 104.857 secs 2005, 17:41:20

Sequence Patent No. Sequence

Sequence 21, Appl
Patent No. 5223424
Sequence 2, Appli
Sequence 17, Appl
Sequence 4, Appli
Sequence 3855, Ap
Sequence 23413, A
Sequence 24, Appl
Sequence 34, Appl
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Total number of hits satisfying chosen parameters:
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US-09-807-802A-15
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US-09-807-802A-13
US-09-807-802A-13
US-10-03B-972A-14
US-10-03B-972A-14
US-09-321-589-1
US-10-293-478-1
US-10-293-478-1
US-10-293-532-594B-16
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US-09-533-427-7
US-08-856-841-20
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Sequence 17, Appl Sequence 3, Appl Sequence 3, Appl Sequence 13, Appl Sequence 14, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 16, Appl Sequence 4, Appl Sequence 5, Appl Sequence 29, Appl Sequence 27, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 13, Appl Sequence 13, Appl Sequence 16, App
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Sequence 17, Application US/09807802A

Patent No. 6799237

Patent N
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US-09-022-949-1

US-10-76-397B-4

US-09-107-5397B-4

US-09-248-796A-23413

US-08-469-202-27

US-08-469-202-27

US-08-484-361-34

US-08-384-361-34

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US-08-357-688-6

US-08-357-698-6

US-08-359-554A-4

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Sequence 15, Application US/09807802A

Patent No. 6759237

GENERAL INFORMATION:
APPLICANT: Wilson, James M.
APPLICANT: Wilson, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
LENGTH: 599
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Matches 534;
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ORGANISM: AAV-1
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FILE REFERENCE: GNVPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR APPLICATION NUMBER: PCT/US99/25694
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 736
; TYPE: PRT
; ORGANISM: AAV-1
US-09-807-802A-3
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Best Local Similarity
Matches 534; Conserv
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APPLICANT: Xiao, Weidong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic Acid Sequences,
TITLE OF INVENTION: Vectors and Host Cells Containing Same
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IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
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Pred. No. 1.6e-257;
); Mismatches 0;
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US-09-807-802A-13; Sequence 13, App.; Patent No. 6759;
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; ORGANISM: AAV-1
US-09-807-802A-13
                                                            RESULT 5
US-10-038-972A-15
; Sequence 15, Application
; Patent No. 6962815
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 736
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Best Local Similarity 100.0%;
Matches 534; Conservative 0
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APPLICANT: Xiao, Weldong
TITLE OF INVENTION: Adeno-Associated Virus Serotype I Nucleic
TITLE OF INVENTION: Vectors and Host Cells Containing Same
FILE REFERENCE: GNUPN.031USA
CURRENT APPLICATION NUMBER: US/09/807,802A
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR APPLICATION NUMBER: US 60/107,114
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1998-11-05
PRIOR FILING DATE: 1999-11-02
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APPLICANT: J. Bartlett
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
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Pred. No. 1.6e-257;
Mismatches 0;
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CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 533
TYPE: PRT
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; LENGTH: 598
TYPE: PRT
; ORGANISM: adeno-associated
US-10-038-972A-14
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                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
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Best Local Similarity
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                                                                                    TITLE OF INVENTION: AAV VECTORS AND METHODS FILE REFERENCE: 2835/56996US CURRENT PEPLICATION NUMBER: US/10/038,972A CURRENT FILING DATE: 2002-01-04 PRIOR APPLICATION NUMBER: US 60/260,124 PRIOR PILING DATE: 2001-01-05 NUMBER OF SEQ ID NOS: 18
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APPLICANT: MCARTHUR, JAMES G.
TILE REFERENCE: 39672
FILE REFERENCE: 39672
CURRENT FILING DATE: 1999-05-28
CURRENT FILING DATE: 1999-05-28
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CURRENT APPLICATION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
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CURRENT APPLICATION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
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CURRENT APPLICATION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DETERMINANTS
FILING DATE: 1990-05-28
CURRENT APPLICATION: ADENO-ASSOCIATED VIRUS CAPSID IMMUNOLOGIC DATE: ADENO-AS
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Patent No. 6498244
GENERAL INFORMATION:
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Matches 445; Conservative
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Best Local Similarity
Matches 445; Conserv
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83.3%; Pred. No. 1.4e-218;
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CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/321,589
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 735
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US-10-293-478-1
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Patent No. 6733757
GENERAL INFORMATION:
APPLICANT: PATEL, SALIL D.
APPLICANT: MCARTHUR, JAMES G.
APPLICANT: MCARTHUR, JAMES G.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS
FILE REFERENCE: 39672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 445; Conserv
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                                                                       LYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQPKNMLPGPCYRQQRVSKTKTDNNNSNFT 300
                                                                                                                                                          NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQY 240
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    WTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTALDNVMITD
                                                                                                                                                                                                                    EVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLN
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                                            LYYLSRINTPSGTTTQSRLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNNSEYS
                                                                                                                                    NGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYTFEDVPFHSSYAHSQSLDRLMNPLIDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%; Score 2481.5; DB 2 ilarity 83.3%; Pred. No. 1.4e-218; Conservative 37; Mismatches 51;
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GENERAL INFORMATION:
APPLICANT: J. BATTLELT
APPLICANT: J. BATTLELT
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/36996US
CURRENT APPLICATION NUMBER: US/10/038,972A
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETBION 3.1
SEQ ID NO 13
LENGTH: 735
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US-10-038-972A-13
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; ORGANISM: adeno-associated virus 2 VP1 caspid protien
US-10-038-972A-13
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Best Local Simi
Matches 445;
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                                            PHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVE
                                                                                            EEEIRTTNEVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKI
                                                                                                           EEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKI
                                                                                                                                                           WTGATKYHLNGRDSLVNPGPAMASHKDDEEKFFPQSGVL1FGKQGSEKTNVD1EKVM1TD
IEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                               PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVE
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Pred. No. 1.4e-218;
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    RYLTHHL 544
                                  RYLTRPL 534
                                                                FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT
                                                                               FITQYSTGQVSVEIEWELQXENSKRWNDEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGT
                                                                                                                               RDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTFSSTPVNS
                                                                                                                                               RDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFAS
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CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09532594B Patent No. 6468524
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
                                                                                          OTHER INFORMATION: synthetic construct NAME/KEY: misc feature OTHER INFORMATION: AAV4 capsid protein
                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence; No.
                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                  58.2%;
  65;
Score 1690.5; DB 2;
Pred. No. 3.1e-146;
5; Mismatches 132;
                                                                                                   VP3
                                      DB 2;
    Indels
                                        Length
                                          544;
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    25;
    Gaps
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APPLICANT: Kotin, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THEREOF
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION NUMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 598
TYPE: PRT
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Best Local Similarity
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                                                                                FITQYSTGQVSVEIEWELQKENSKRWNDEVQYTSNYAKSANVDETVDNNGLYTEPRPIGT
                                                                                                                                               RDVYLQGPIWAKIPHTDGHFHSSPLMGGFGLKNEPPQILIKNTPVPANPPAEFSATKFAS
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RYLTHHL 598
                              RYLTRPL 534
                                                                                                                              RDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKHPPPQIFIKNTPVPANPATTFSSTPVNS
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                                                               FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT
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Pred. No. 3.6e-146;
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Sequence 4, Application US/09532594B
PAtent No. 6468524
GENERAL INFORMATION:
APPLICANT: Chorini, John A.
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Safer, Brian
APPLICANT: Davidson, Beverly
TITLE OF INVENTION: AAV4 VECTOR AND USES THER
FILE REFERENCE: 14014.0252U2
CURRENT APPLICATION UNMBER: US/09/532,594B
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 734
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Best Local
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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728
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 RYLTHHL 734
                               RYLTRPL 534
                                                                   FITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNYGQQNSLLWAPDAAGKYTEPRAIGT
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizabeth
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BRAFILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEG ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEG ID NO 6
LENGTH: 532
TYPE: PRT
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Matches 318;
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Patent No. 6855314
GENERAL INFORMATION:
                                                          Sequence 5, Application US/09533427
Patent No. 6855314
GENERAL INFORMATION:
APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Davidson, Elizab
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Pred. No. 6.5e-144;
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APPLICANT: Chiorini, John
APPLICANT: Kotin, Robert M.
APPLICANT: Safer, Brian
APPLICANT: Bafer, Brian
APPLICANT: Zabner, Joseph
APPLICANT: Zabner, Joseph
TITLE OF INVENTION: AAV5 VECTOR FOR TRANSDUCING BR.
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23

BRAIN CELLS

AND LUNG

CELLS

SOFTWARE: FastSEQ

for Windows Version

US-09-533-427-4

GENERAL INFORMATION:

Sequence 4, Application US/09533427 Patent No. 6855314

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TITLE OF INVENTION: AAUS VECTOR FOR TRANSDUCING BRAIN CELLS AND
FILE REFERENCE: 14014.0323U2
CURRENT APPLICATION NUMBER: US/09/533,427
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 23
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 588
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE: REPOWATION: Description of Artificial Sequence:/No. 6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                  NMLITSESETQPVNRVAYNVGGOMATNNQSSTTAPATGTYNLQEIVPGSVWMERDVYLQG
                                                                                                                                       NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
                                                                                                                                                                              VSAFATTNRMELEGASYQVPPQPNGMTNNLQGSNTYALENTM1FNSQPANPGTTATYLEG
                                                                                                                                                                                                              NFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTAL---D
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              GQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL
                                                          PIWAKIPETGAHFHPSPAMGGFGLKHPPPMMLIKNTPVPGN-ITSFSDVPVSSFITQYST
                                                                           PIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPANPPAEFSATKFASFITQYST
GOVTVEMEWELKKENSKRWNPEIQYTNNYNDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL
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Pred. No. 7.6e-144;
4; Mismatches 154;
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LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. 6855314e
OTHER INFORMATION: synthetic construct
(S-09-533-427-4
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Best Local Similarity
Matches 318; Conserv
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                                PIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPGN-ITSFSDVPVSSFITQYST
NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDVYLQG
                                                                                                                                               QYLYYLNRTQNQSGSAQNKDLLFSRGSPAGMSVQP-KNWLPGPCYRQQRVSKTKTDNNNS
                                                                                                                                                                                                     NMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQBIVPGSVWMERDVYLQG
                                                                                                    VSAFATTNRMELEGAS YQVPPQPNGMTNNLQGSNTYALENTMI FNSQPANPGTTATYLEG
                                                                                                                     NFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPMSGVMIFGKESAGASNTAL---D
                                                                                                                                      QYLYRFVSTNNTGGVQFNKNL-----AGRYANTYKNWFPGPMGRTQGWNLGSGVNRAS
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Search completed: November 23, 2005, 17:42:49 Job time : 25.2857 secs